

## SUPPLEMENTARY INFORMATION

### Systematic identification of genomic markers of drug sensitivity in cancer cells

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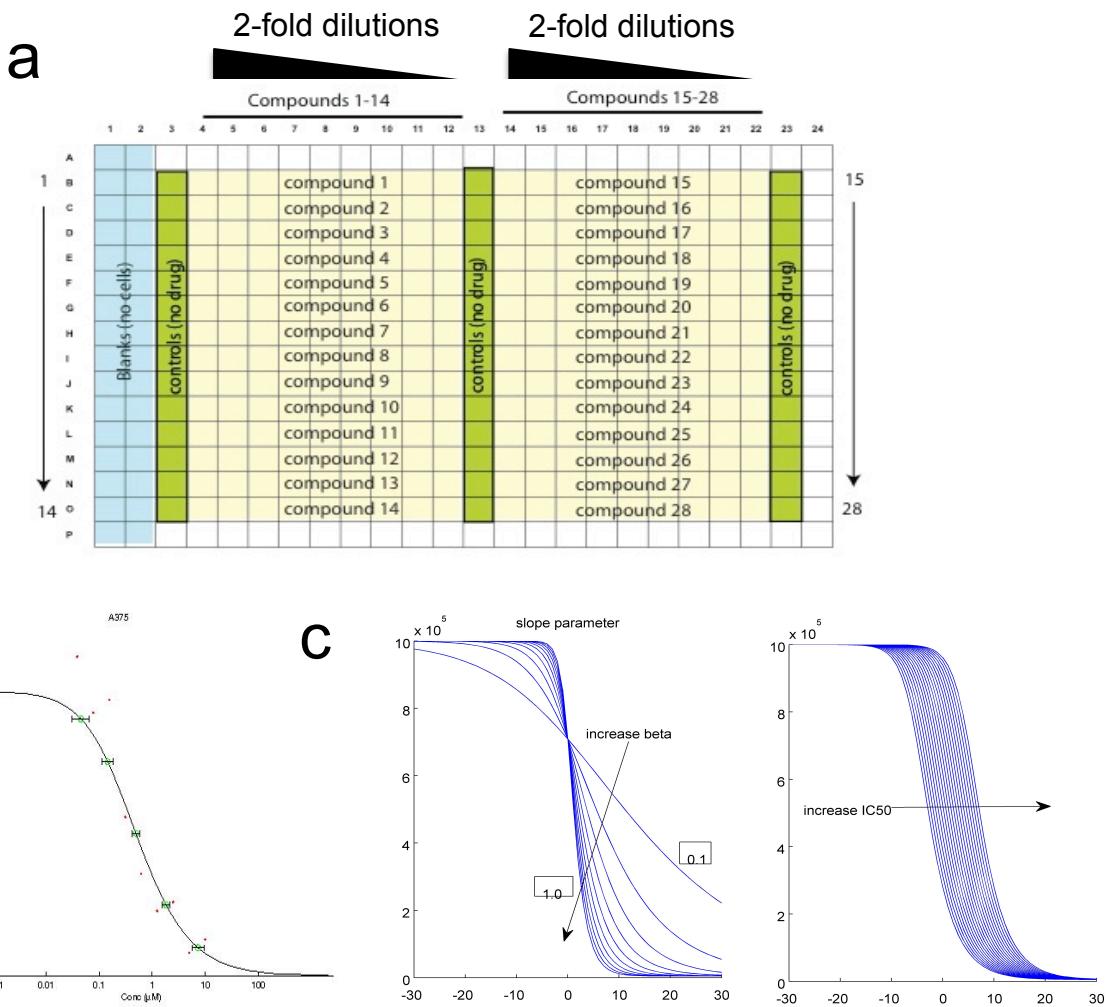
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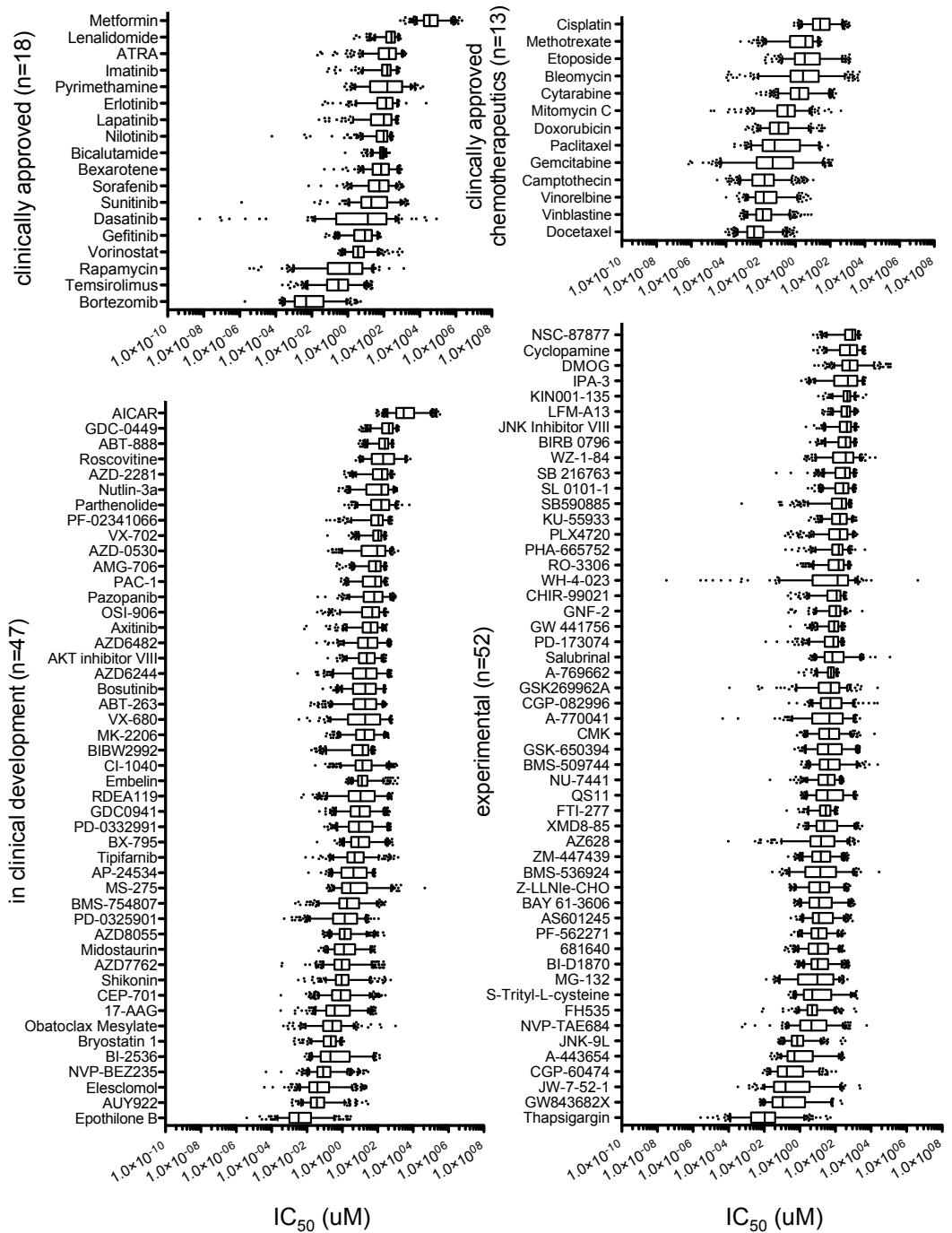
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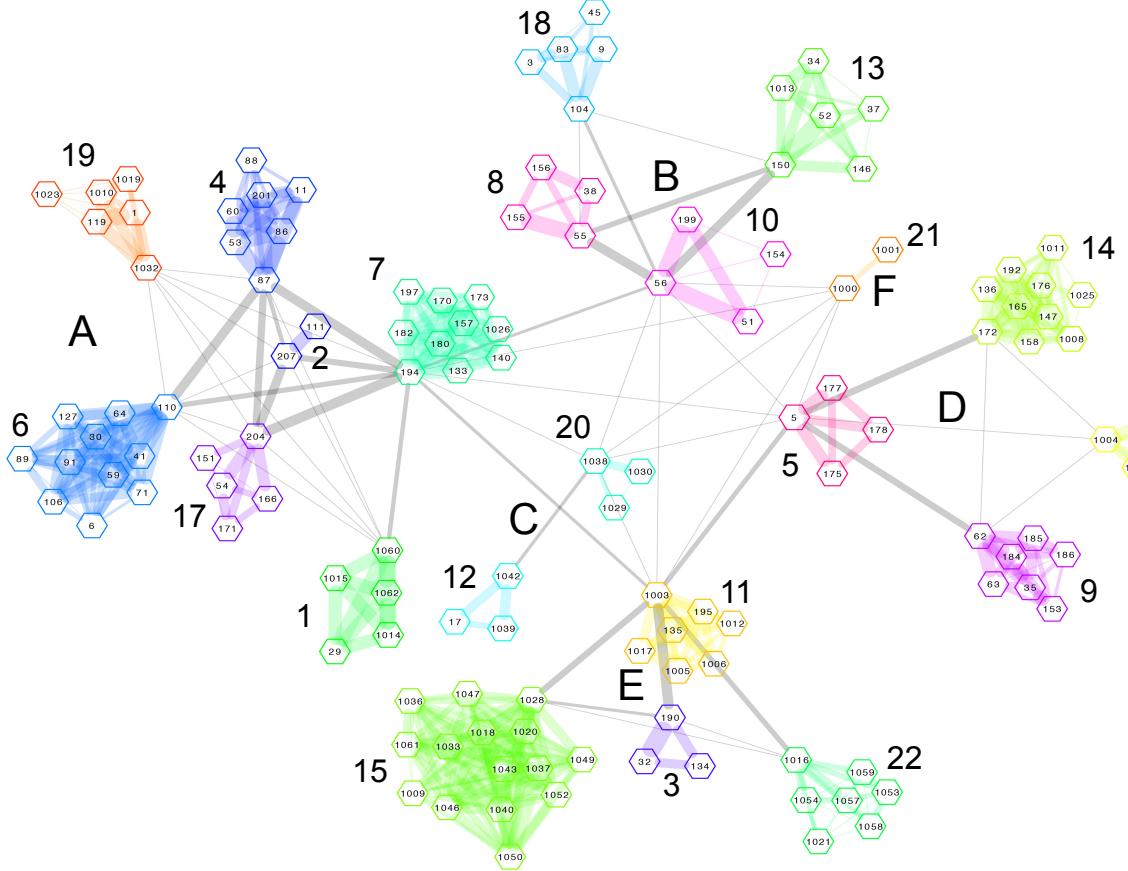
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**Supplementary Figure 1: Screening format and curve-fitting algorithm.** **a**, A schematic diagram of a typical 384-well screening plate. A single cell line is used on each plate and treated with 28 different drugs over a 9-pt, 256-fold concentration range. Wells with no cells (blanks) and untreated wells (controls) are used as controls on each plate. **b**, An example of curve-fitting of drug sensitivity data to generate a multi-parameter description of drug response. Red circles are normalized screening data and the curve fit is shown. Green circles represent  $\text{IC}_{10}$ ,  $\text{IC}_{25}$ ,  $\text{IC}_{50}$ ,  $\text{IC}_{75}$  and  $\text{IC}_{90}$  values and error bars are confidence intervals. **c**, Representations of output parameters calculated from the curve-fitting algorithm. The slope parameter (beta) and  $\text{IC}_{50}$  value from the dose-response curve are shown.



**Supplementary Figure 2: Cell line sensitivity across the drug collection.** Drugs are classified as clinically approved, clinically approved chemotherapeutics, in clinical development or experimental. For each drug the range of cell line IC<sub>50</sub> values is represented as a box and whisker plot. The median IC<sub>50</sub>, interquartile ranges, and 95% confidence intervals are shown for each drug. Outlier cell line IC<sub>50</sub>s are indicated by black dots.



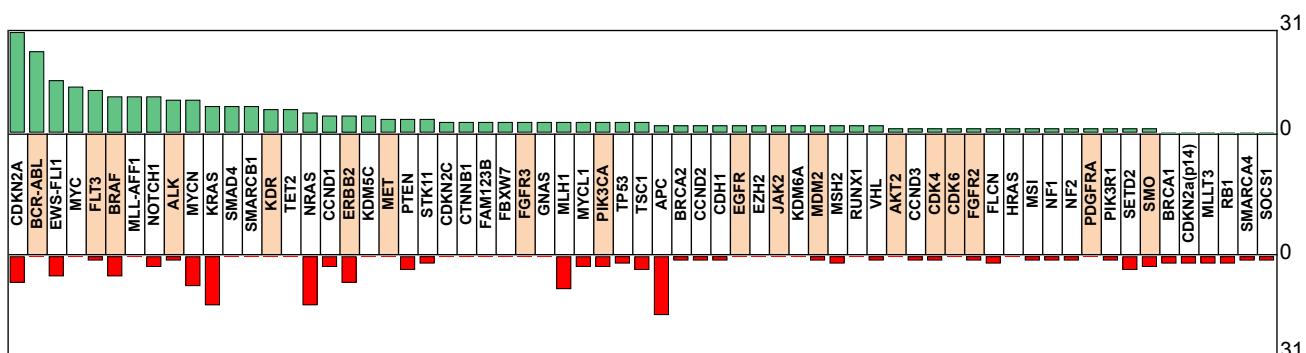
**Supplementary Figure 3: Clustering of drugs based on  $IC_{50}$  values.** A network visualization of drug similarity based on cell line  $IC_{50}$  values. Drugs are clustered in 22 communities (1-22) and 6 “communities of communities” (A-F, rich clubs) dependent on their intra and inter cluster correlations, respectively. An ID number identifies individual drugs and the thickness of an edge is proportional to the similarity of the connected nodes and different colors indicate different clusters. Node positions roughly reflect drug similarities (i.e. the closer two nodes are the more correlated the  $IC_{50}$  patterns of the corresponding drugs are) and have been computed through the “spring-embedding” algorithm for network layout.

C	total Avg Corr	odd Ratio	Drug id	Avg Corr	Drug Generic Name	Drug Target	C	total Avg Corr	odd Ratio	Drug id	Avg Corr	Drug Generic Name	Drug Target
1	0.7338 5.8277	1060 0.8162 1062 0.7999 1014 0.7961 29 0.7644 1015 0.7585	PD-0325901 * AZD6244 RDEA119 A2628 CI-1040	MEK1/2 MEK1/2 MEK1/2 BRAF MEK1/2	13 0.4602 3.6161	150 0.6569 52 0.6457 34 0.5551 146 0.4924 37 0.4195	Bicalutamide * GNF-2 Imatinib Nilotinib A-769662 PF-2341066	Androgen receptor BCR-ABL ABL, KIT, PDGFR ABL AMPK MET, ALK					
									XIAP				
									SHP1/2				
									Prolyl-4-Hydroxylase				
									PAK				
2	0.6960 5.5745	207 0.8480 111 0.8480	AS601245 * Salubrin	JNK GADD34-PP1C phosphatase	14 0.4362 3.4325	172 0.5933 147 0.5606 165 0.5532 176 0.5527 158 0.5477 136 0.5239 192 0.4787 1008 0.4575 1011 0.3896 1025 0.2685	Embelin * NSC-87877 DMOG IPA-3 PF-562271 Mitomycin LFM-A13 Methotrexate ABT-263 SB 216763	XAP SHP1/2 DNA crosslinker BTK Dihydrofolate reductase (DHFR) BCL2, BCL-XL, BCL-W GSKa/b					
									FAK				
									DNA crosslinker				
									BTK				
									Dihydrofolate reductase (DHFR)				
3	0.6600 5.1446	190 0.8164 32 0.8077 134 0.6958	Bleomycin * VX-680 Etoposide	Aurora A/B/C, FLT3, ABL1, JAK2, TOP2	15 0.4296 3.3583	1028 0.5844 1043 0.5728 1046 0.5212 1037 0.5187 1040 0.5150	VX-702 * JNK Inhibitor VIII 681640 BX-795 BI-D1870	p38 MAPK JNK WEE1, CHK1 TBK1, PDK1, IKK, AURKB/C RSK1/2/3/5, PLK1, AURKB					
									AURKB				
									PARP1/2				
									BRaf				
									TNF alpha				
4	0.6409 5.0275	87 0.7933 60 0.7861 86 0.7402 201 0.7302 53 0.7286 11 0.6501 88 0.4169	GW843682X * BI-2536 A-443654 Epothilone B CGP-60474 Paclitaxel MS-275	PLK1 PLK1/2/3 AKT1/2/3 Microtubules CDK1/2/5/7/9 Microtubules HDAC	16 0.4252 3.3359	1050 0.5146 1018 0.4974 1046 0.5212 1037 0.5187 1040 0.5150	ZM-47439 ABT-888 SB590885 Lenalidomide PD-173074 RO-3306 PLX4720 Nutlin-3a GDC-0449 ATRA	p38 MAPK JNK WEE1, CHK1 TBK1, PDK1, IKK, AURKB/C RSK1/2/3/5, PLK1, AURKB					
									AURKB				
									PARP1/2				
									BRaf				
									TNF alpha				
5	0.5500 4.3118	5 0.7202 177 0.6586 175 0.6372 178 0.6339	Sunitinib * GSK-650394 PAC-1 BAY 61-3606	PDGFRA, PDGFRB, KDR, KIT, FLT3 SGK3 CASP3 activator SYK	17 0.4215 3.3315	1050 0.5146 1018 0.4974 1046 0.5212 1037 0.5187 1040 0.5150	ZM-47439 ABT-888 SB590885 Lenalidomide PD-173074 RO-3306 PLX4720 Nutlin-3a GDC-0449 ATRA	p38 MAPK JNK WEE1, CHK1 TBK1, PDK1, IKK, AURKB/C RSK1/2/3/5, PLK1, AURKB					
									AURKB				
									PARP1/2				
									BRaf				
									TNF alpha				
6	0.5327 4.1633	110 0.6801 59 0.6578 91 0.6259 41 0.6087 30 0.6008 30 0.5917 64 0.5879 127 0.5824 71 0.5208 89 0.4621 6 0.4089	Roscovitine * WZ-1-84 KIN001-135 S-Trityl-L-cysteine Sorafenib XMD8-85 CMK GSK269962A Pyrimethamine Parthenolide PHA-665752	CDK5 BMX IKK KIF11 ERKS RSK ROCK STAT3 NFKappaB MET	18 0.4296 3.3583	1050 0.5146 1018 0.4974 1046 0.5212 1037 0.5187 1040 0.5150	ZM-47439 ABT-888 SB590885 Lenalidomide PD-173074 RO-3306 PLX4720 Nutlin-3a GDC-0449 ATRA	p38 MAPK JNK WEE1, CHK1 TBK1, PDK1, IKK, AURKB/C RSK1/2/3/5, PLK1, AURKB					
									AURKB				
									PARP1/2				
									BRaf				
									TNF alpha				
7	0.5266 4.1296	194 0.6685 180 0.6399 157 0.6184 182 0.6082 133 0.5978 140 0.5865 170 0.5530 173 0.5296 197 0.4869 1026 0.4505	NVP-AU922 * Thapsigargin JNK-9L Obatoclax Mesylate Doxorubicin Vinorelbine Shikonin FH535 Bryostatin 1 17-AAG	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 BCL-2, BCL-XL, MCL-1 DNA intercalating Microtubules unknown 	19 0.3659 2.8674	1028 0.5844 1043 0.5728 1046 0.5212 1037 0.5187 1040 0.5150 1031 0.4464	VX-702 * JNK Inhibitor VIII 681640 BX-795 BI-D1870 Elesclomol HSP70	p38 MAPK JNK WEE1, CHK1 TBK1, PDK1, IKK, AURKB/C RSK1/2/3/5, PLK1, AURKB					
									AURKB				
									PARP1/2				
									BRaf				
									TNF alpha				
8	0.5182 4.0438	55 0.6868 155 0.6437 156 0.6259 38 0.5982	SRC family AP-24534 ABL PI3Kb SRC, ABL1	SRC family ABL, KIT, PDGFR PI3Kb SRC, ABL1	20 0.4095 3.2365	104 0.6108 1024 0.5860 1007 0.5537 1022 0.5039 1031 0.4464	Bortezomib * CEP-701 Docetaxel Elesclomol HSP70	Proteasome MTOR MTOR Proteasome g-secretase					
									Proteasome				
									MTOR				
									MTOR				
									g-secretase				
9	0.5055 3.9489	62 0.6946 184 0.6846 35 0.6378 185 0.5832 153 0.5137 63 0.4895 186 0.4296	BMS-536924 * BMS-754807 NVP-TAE684 IGF1R OSI-906 Midostaurin BMS-509744 Bexarotene	IGF1R IGF1R ALK IGF1R KIT ITK Retinoic acid X family agonist	19 0.3659 2.8674	1032 0.5838 1 0.5620 119 0.5479 1010 0.4803 1019 0.4036 1023 0.2519	BIBW2992 * Erlotinib Lapatinib Gefitinib Bosutinib GW-441756	EGFR, ERBB2 EGFR EGFR, ERBB2 SRC, ABL, TEC NTRK1					
									EGFR				
									ERBB2				
									EGFR				
									SRC, ABL, TEC				
10	0.4931 3.8986	56 0.7207 51 0.6816 199 0.6571 154 0.4200	WH-4-023 * Dasatinib Pazopanib CHIR-99021	SRC family ABL, KIT, PDGFR VEGFR, PDGFR, PDGFR, KIT GSK3b	20 0.3555 2.7617	1038 0.6160 1030 0.5744 1029 0.5206	NU-7441 * KU-55933 AMG-706	DNAPK ATM VEGFR, RET, c-KIT, PDGFR					
									DNAPK				
									ATM				
									VEGFR, RET, c-KIT, PDGFR				
									AMPK				
11	0.4826 3.7883	1003 0.6594 195 0.6083 135 0.5947 1006 0.5309 1017 0.5292 1005 0.5141 1012 0.4587	Camptothecin * Camptothecin Gemcitabine Cytarabine AZD-2281 Cisplatin Vorinostat	TOP1 TOP1 DNA replication Inhibits DNA synthesis PARP1/2 DNA crosslinking HDAC inhibitor Class I, IIa, IIb, IV	21 0.3465 2.7612	1016 0.4957 1057 0.4629 1053 0.3970 1054 0.3943 1058 0.3583 1059 0.3444 1021 0.3093	Temsirolimus * NVP-BEZ235 MK-2206 Gefitinib Bosutinib GDC0941 Axitinib	mTOR PI3K Class 1 and mTORC1/2 AKT1/2 CDK4/6 PI3K class 1 mTORC1/2 PDGFR, KIT, VEGFR					
									mTOR				
									PI3K Class 1 and mTORC1/2				
									AKT1/2				
									CDK4/6				
12	0.4838 3.7723	1042 0.6823 1039 0.6489 17 0.6364	BIRB 0796 * SL 0101-1 Cyclophamine	p38, JNK2 RSK, AURKB, PIM3 SMO	22 0.2936 2.2959	1000 0.6733 1001 0.6733	Metformin * AICAR	AMPK AMPK					
									AMPK				

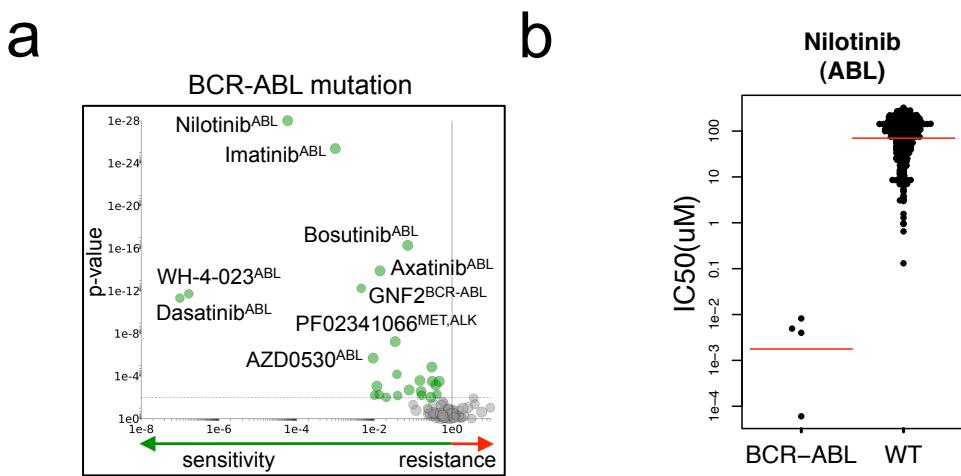
\* community exemplars

	1	2	4	6	7	17	19	8	10	13	18	12	20	5	9	14	16	3	11	15	22	21	
1				0.2395	0.3477									-0.8813		-0.1916						-0.1384	
2				0.2643		0.2544	0.2856											0.3422					
4				0.2643		0.3428	0.4440	0.4665							0.3163	-0.9376						A	
6	0.2395			0.3428		0.3112	0.2756		0.2756					-0.9193	0.2385	-0.2777							
7	0.3477	0.2544	0.4440	0.3112		0.3194			0.2434	-0.1268		-0.2788		-0.5656	0.2349	-0.3827							
17				0.2856	0.4665	0.2756	0.3194								-0.6515								
19								-0.5179		-0.1130				-0.4989	-0.2494	-0.3555						-0.1291	
8				0.2756	0.2434	0.2657	0.2778					0.4260	0.2723			-0.1537						-0.5998	
10					-0.1268		-0.5179	0.4260		0.2947	0.2415											B	
13								0.2723	0.2947														
18					-0.2788		-0.1130		0.2415													-0.1468	
12												0.2812											C
20																							D
5	-0.8813					-0.9193	-0.5656	-0.4989						0.2664	0.4177			0.3689	0.3544				
9				0.3163	0.2385	0.2349		-0.2494						0.2664				0.2365				-0.2956	
14	-0.1916			-0.9376	-0.2777	-0.3827	-0.6515	-0.3555	-0.1537					0.4177				0.1990				0.3117	
16																		0.2698	-0.6500	0.2296			
3				0.3422	0.3928		0.3265	0.3382						0.3689				0.4197				E	
11							0.2496	-0.1778						0.3544	0.2365	0.1990	0.2698	0.4197	0.2762				
15								-0.4549		-0.1846								-0.6500		0.2296		-0.3716	
22																						F	
21	-0.1384			-0.1291		-0.5998		-0.1468						-0.2956	0.3117								
	A	B	C	D	E	F																	

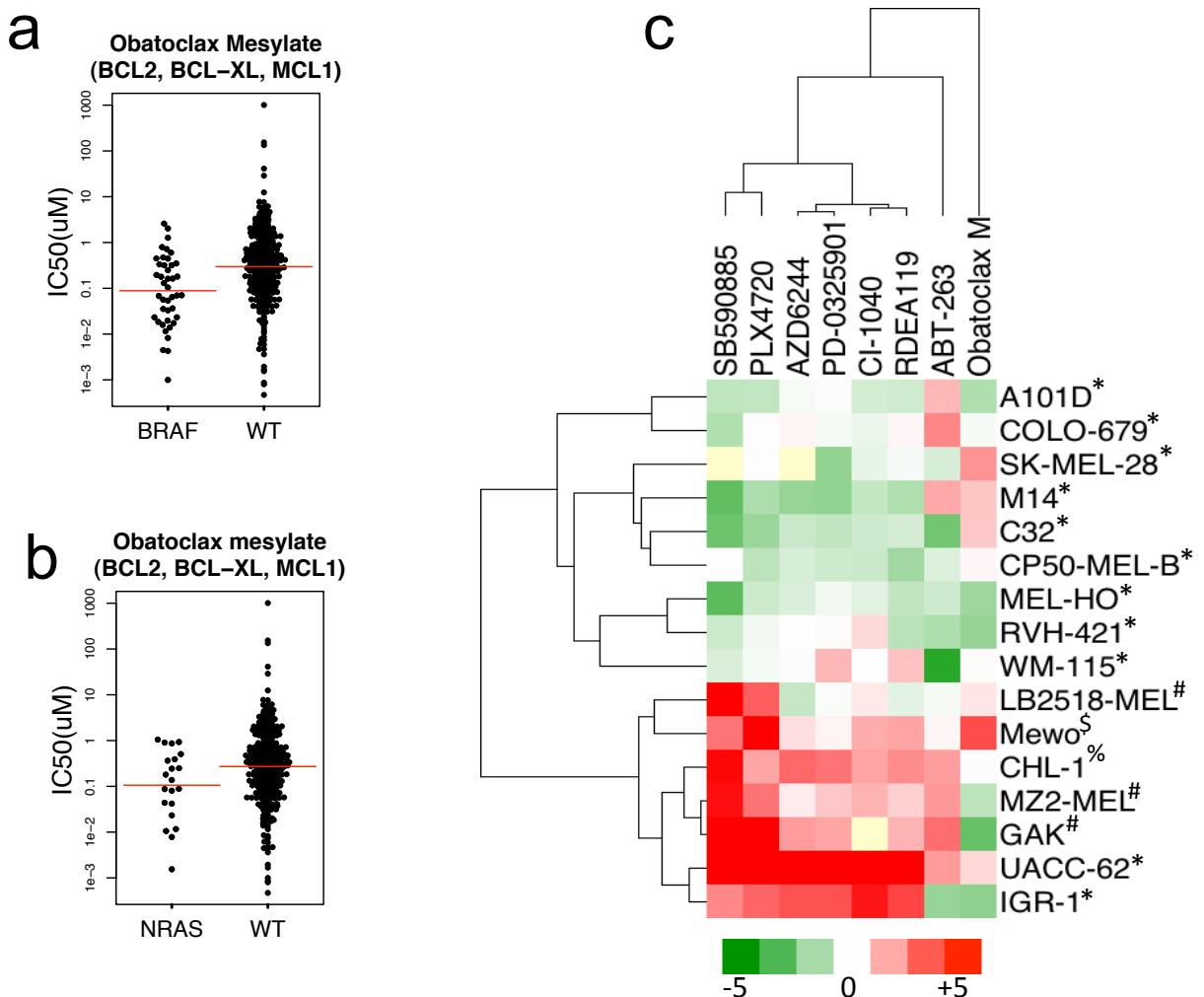
**Supplementary Table 2: Cluster-to-cluster similarity scores and rich-club compositions.** The inter-cluster similarity score is provided for each pair of communities and quantifies the extent of their similarity. Green values indicates positive similarities (correlations) while red values indicate "negative" ones (anti-correlations). Only significant values ( $P < 0.05$ ) were included and communities (1 - 22) were grouped to reflect the rich-club compositions (A - F).



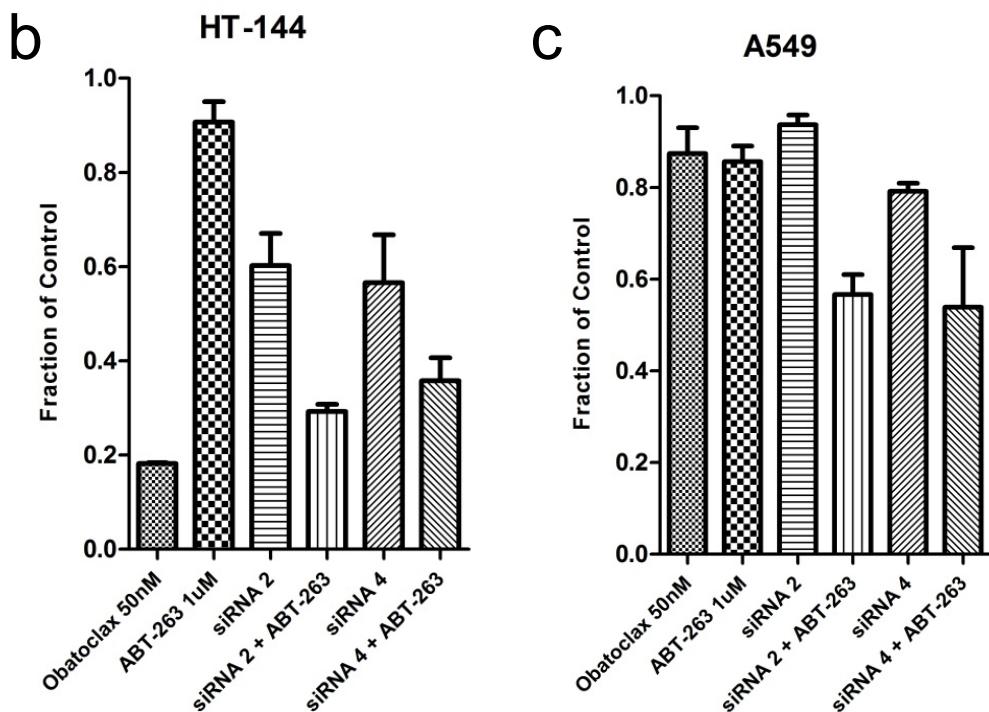
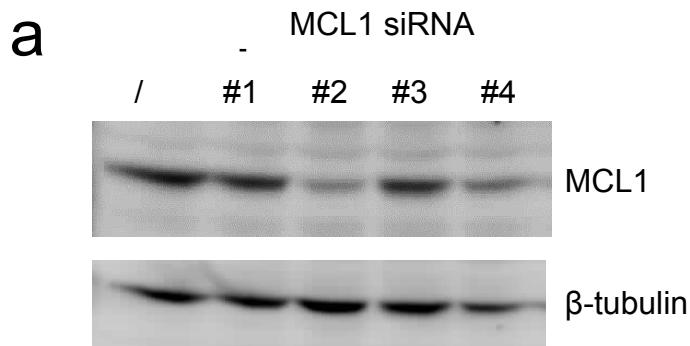
**Supplementary Figure 4: The majority of cancer genes are associated with drug response.** The number of statistically significant sensitizing (green bars) or resistance (red bars) associations identified by MANOVA for each cancer gene. Genes that are reported to be the direct target of a screening drug are coloured. The following genes were analysed but were not associated with drug response: *IDH1*, *MAP2K4*, *KIT*, *MSH6*. Drug response was also correlated with microsatellite instability (MSI) status.



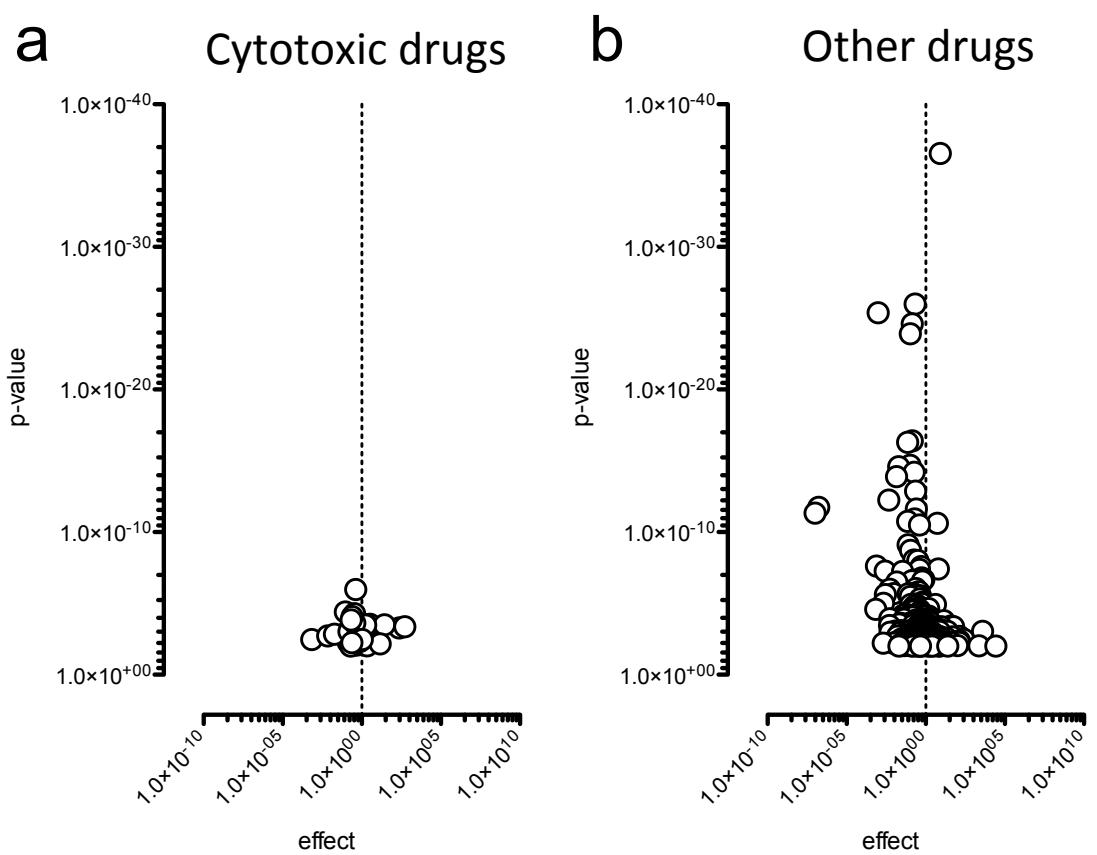
**Supplementary Figure 5: The *BCR-ABL* rearrangement is associated with sensitivity to multiple ABL inhibitors.** **a**, A gene-specific volcano plot from the MANOVA showing the magnitude (effect; x-axis) and significance (p-value; inverted y-axis) of drug sensitivity associated with *BCR-ABL* mutations in cancer cell lines. Each circle represents a single drug interaction and for selected associations the drug name and therapeutic drug target(s) (in superscript) are indicated. A horizontal dashed line indicates the threshold of statistical significance (0.2 FDR,  $P < 0.0099$ ) and significant associations with drug sensitivity are coloured green. *BCR-ABL* was not associated with drug resistance. For clarity, the p-value for nilotinib ( $P = 2.54 \times 10^{-65}$ ) has been capped at  $1 \times 10^{-28}$ . **b**, A scatter plot of *BCR-ABL* mutated or wild-type (WT) cell line IC<sub>50</sub> values for nilotinib. Each circle represents the IC<sub>50</sub> of one cell line on a log scale and the red bar is the geometric mean.



**Supplementary Figure 6: BRAF and NRAS mutations are markers of melanoma sensitivity to obatoclax mesylate.** **a** and **b**, Scatter plots from screening data of obatoclax mesylate IC<sub>50</sub> values of **a**, BRAF or **b**, NRAS mutated versus wild-type (WT) cell lines. The p-values from the MANOVA analysis for these associations are  $P = 1.4 \times 10^{-4}$  and  $P = 0.0055$  for BRAF and NRAS, respectively. Each circle represents the IC<sub>50</sub> of one cell line on a log scale and the red bar is the geometric mean. **c**, A heatmap comparing sensitivity of melanoma cell lines to obatoclax mesylate, ABT-263, BRAF inhibitors (PLX4720, SB590885), MEK1/2 inhibitors (AZD6244, PD-0325901, CI-1040, RDEA119). Sensitivity to obatoclax is not correlated with sensitivity to MEK or BRAF inhibitors. The colour scale corresponds to median centered natural log (IC<sub>50</sub>) values. Mutational status is indicated as follows: \*, BRAF V600; #, NRAS; \$, NF1; %, KRAS amplified.

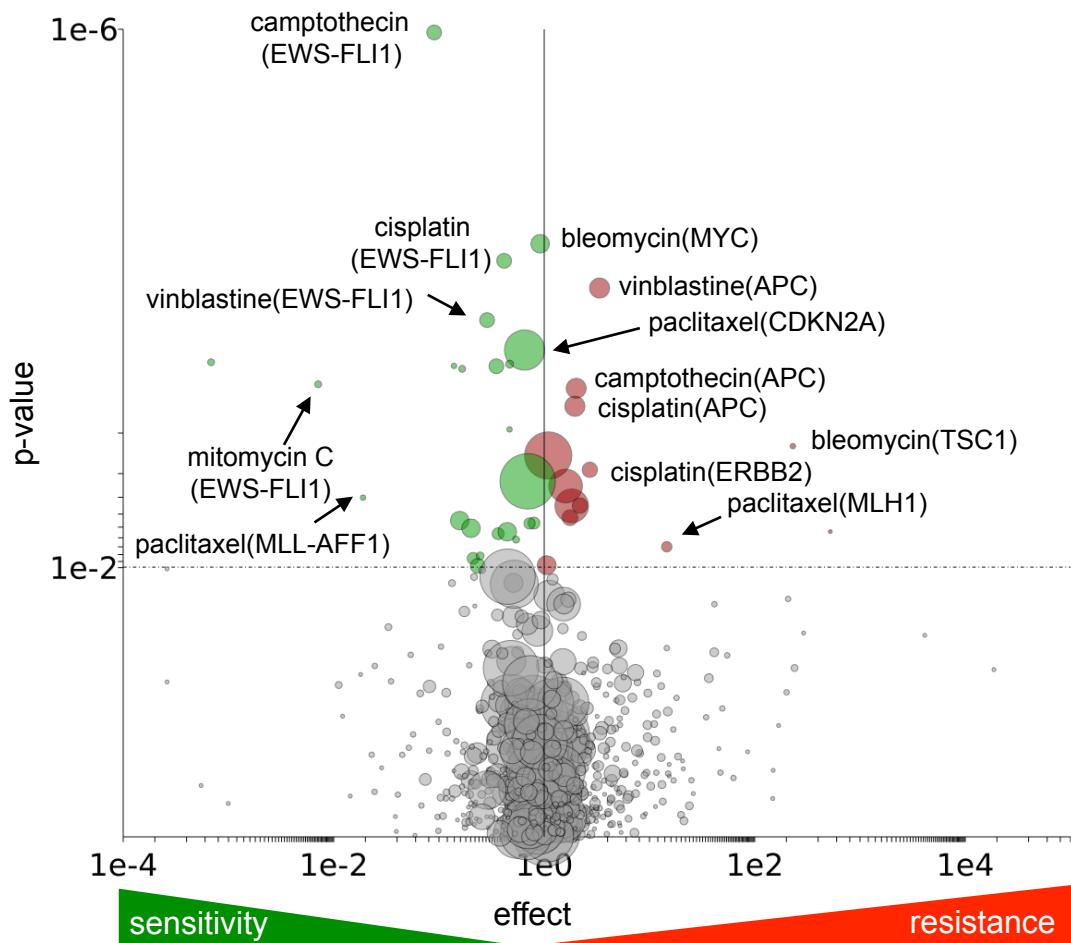


**Supplementary Figure 7: MCL1 knockdown sensitises melanoma cells to ABT-263.** **a**, Western blot of MCL1 protein levels in mock transfected cells or following 72 hr knockdown with multiple MCL1 siRNA. siRNA #2 and #4 gave the most efficient knockdown and were selected for subsequent cell viability assays. **b** and **c**, Effect on the cell viability of the *BRAF* (V600E) mutant HT-144 melanoma cell line after 72 hour treatment with obatoclax (50 nM), or ABT-263 (1  $\mu$ M) alone or together with 40 nM MCL1 siRNA. The lung cancer cell line A549 which is wild-type for *BRAF* was used as negative control. Cell viability was assayed in triplicate and error bars represent standard deviations.

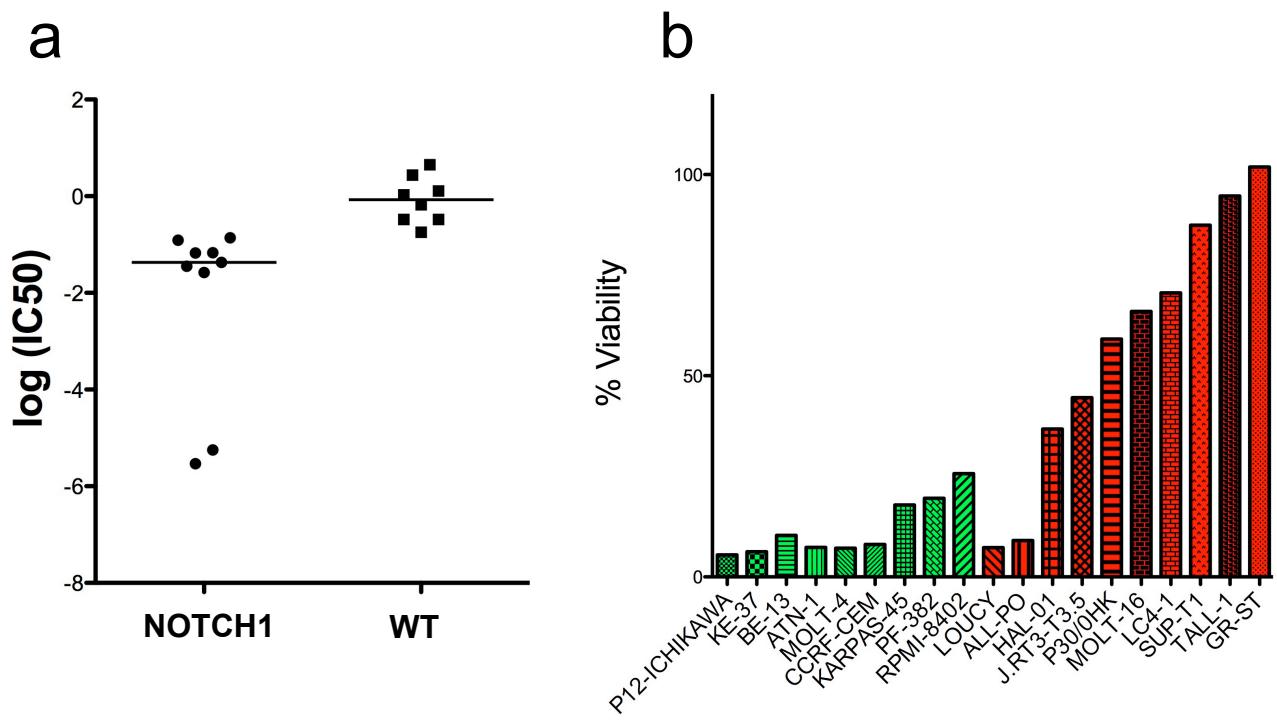


**Supplementary Figure 8: Cytotoxic chemotherapeutic drugs were not associated with highly significant genomic correlations.** Volcano plots showing the effect size (x-axis) and p-value (y-axis, inverted scale) of statistically significant associations identified by the MANOVA. **a**, Cytotoxic drugs ( $n=13$ ) were correlated with 41 associations and **b** the remaining drugs ( $n=117$ ) with 407 associations. For clarity the association between nilotinib and *BCR-ABL* ( $P = 2.45 \times 10^{-65}$ ) has been excluded from **b**.

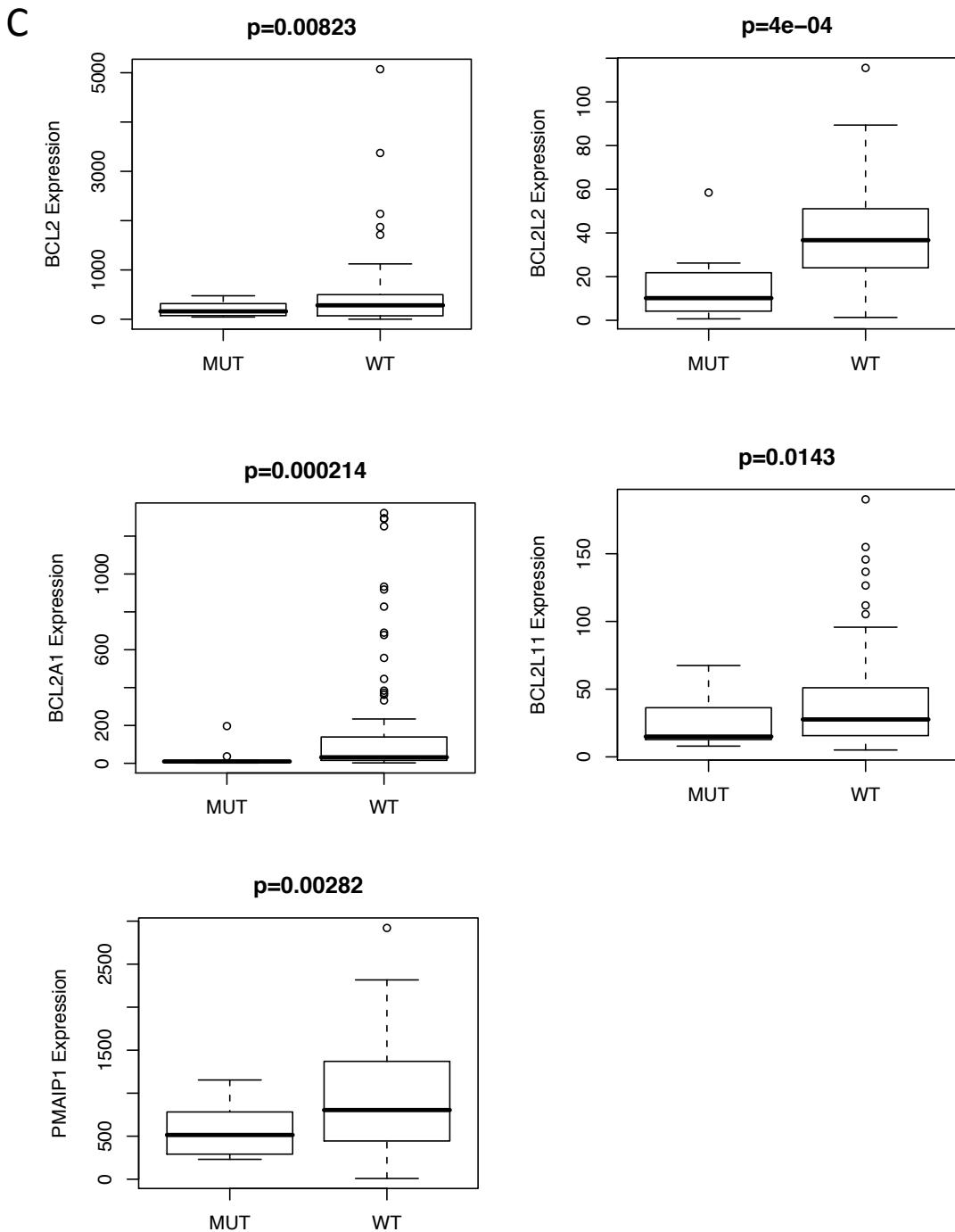
## Cytotoxic drugs



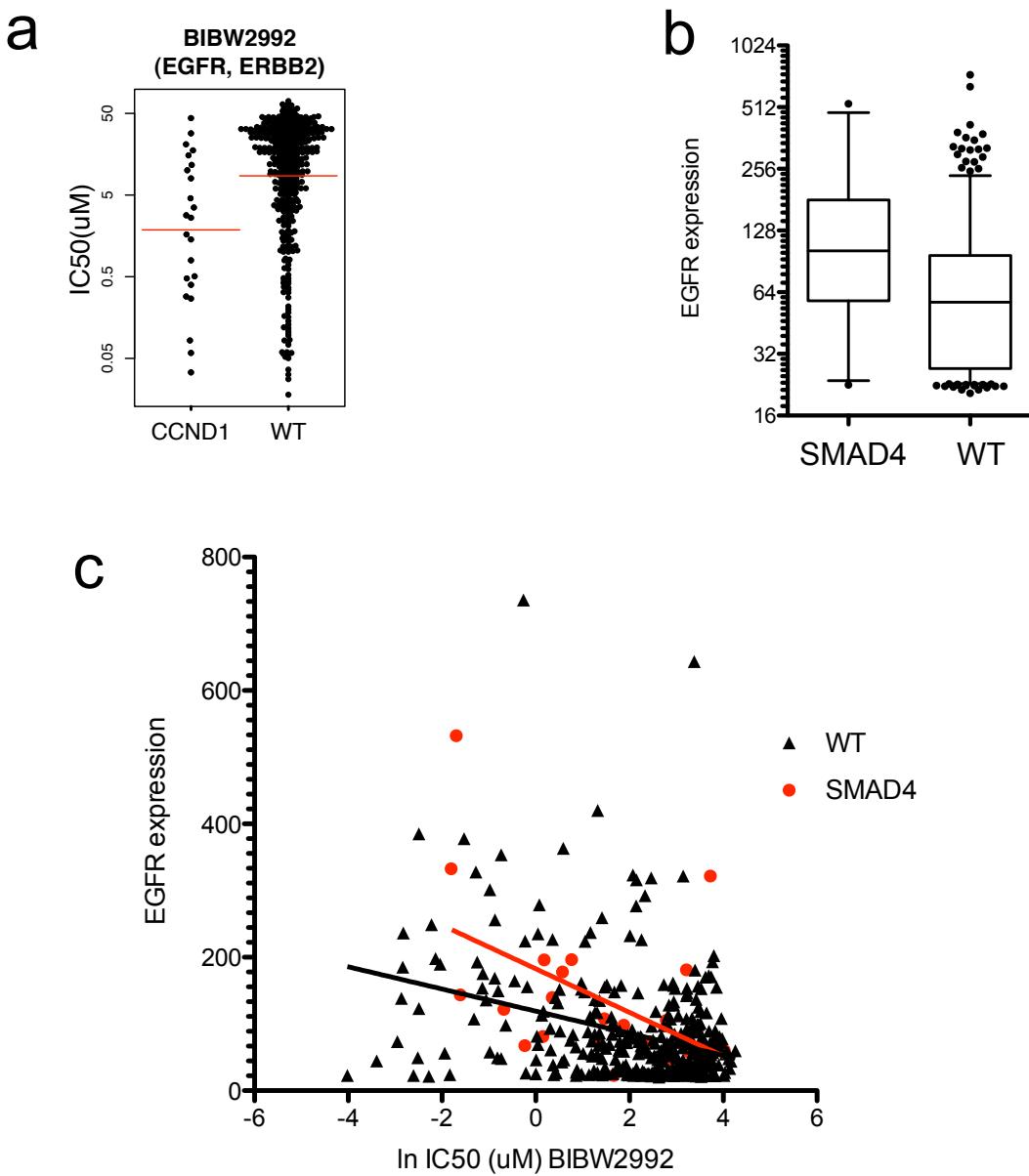
**Supplementary Figure 9: Genomic markers of sensitivity to cytotoxic chemotherapeutics.**  
A volcano plot representation of cytotoxic drugs ( $n = 13$  drugs) from the MANOVA showing the magnitude (effect; x-axis) and significance (p-value; inverted y-axis) of all drug-gene associations. Each circle represents a single drug-gene interaction and the circle size is proportional to the number of mutant cell lines screened (maximum = 312). The horizontal dashed line indicates the threshold of statistical significance (0.2 FDR,  $P < 0.0099$ ) and significant associations with drug sensitivity or resistance are coloured green and red, respectively. Select significant drug-gene associations are labeled with drug name and gene name (bracketed).



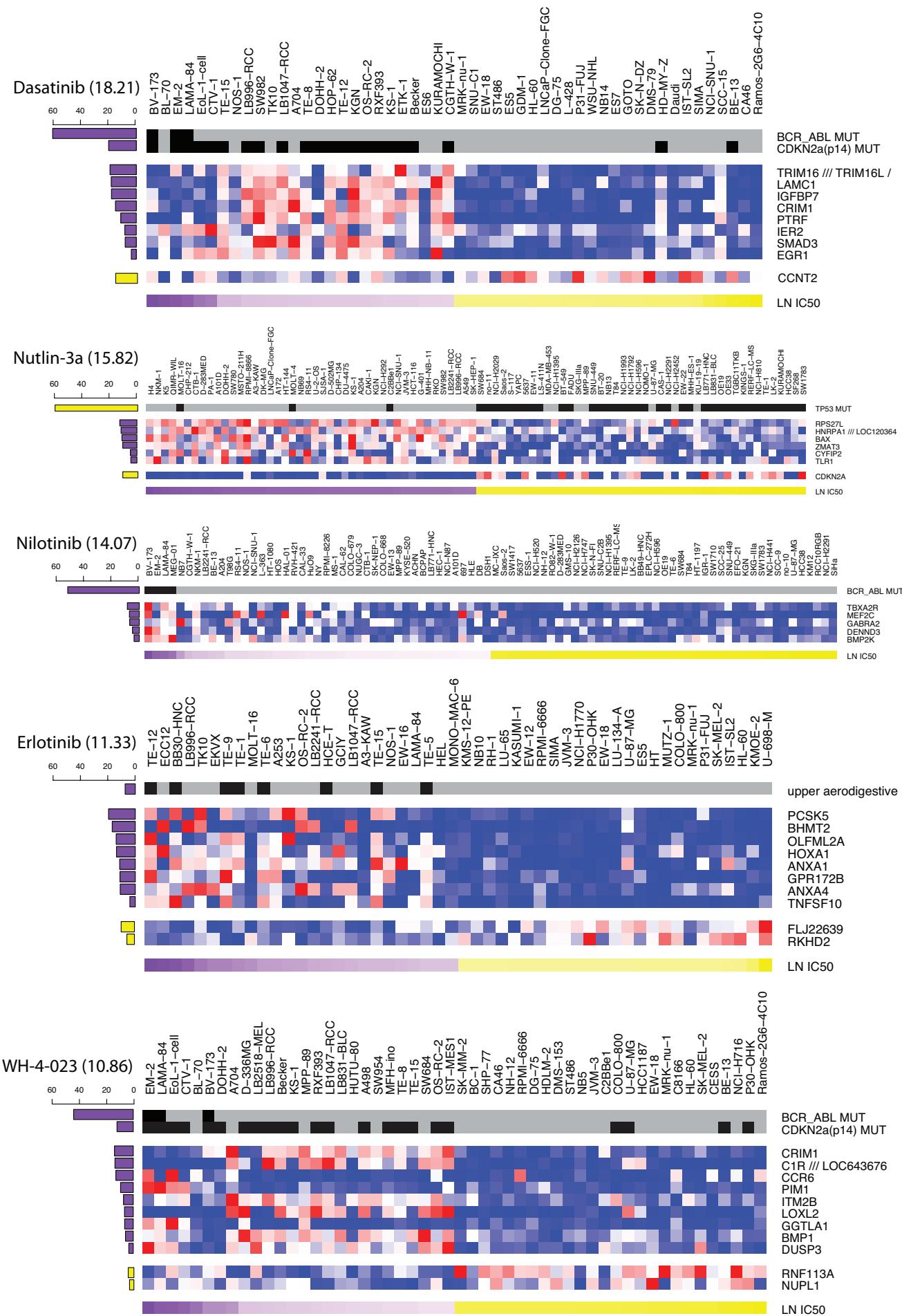
**Supplementary Figure 10: Sensitivity of NOTCH1 mutant leukemic cell lines to ABT-263 following 7 day drug treatment.** A panel of leukemic lines (9 NOTCH1 mutant and 8 wild-type) were treated for 7 days with increasing concentrations of ABT-263 (40 nM – 10 uM). **a**, The concentration of ABT-263 necessary to obtain 50% reduction in cell number ( $\text{IC}_{50}$ ) was determined to be significantly lower for NOTCH1 mutant lines ( $P < 0.0001$ , student t-test) than wild-type (WT) lines. **b**, Normalised cell viability following 7 days of treatment with 0.31 uM ABT-263 for NOTCH1 mutant (green fill,  $n = 9$ ) and wild-type (red fill,  $n = 10$ ) cell lines.

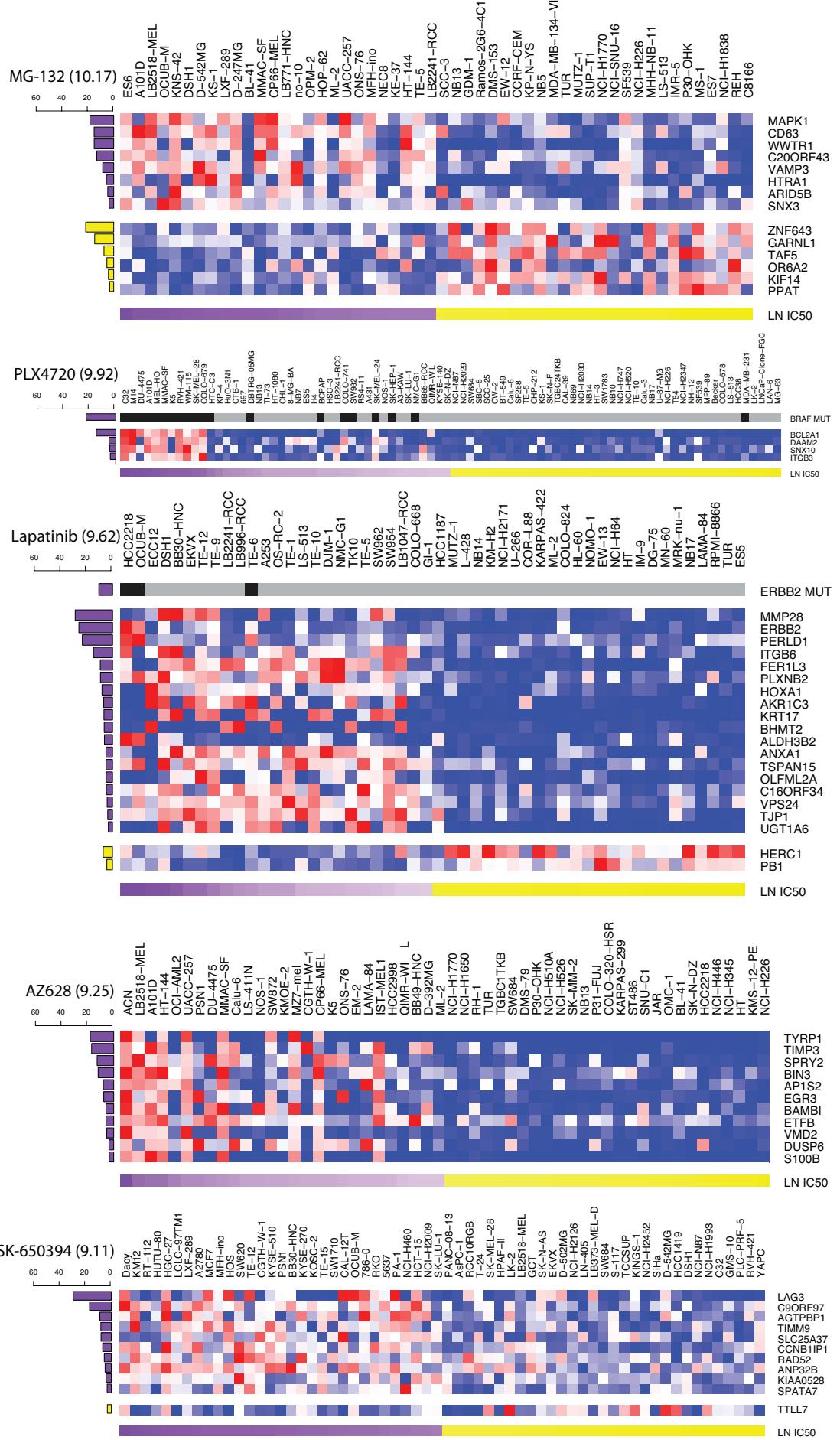


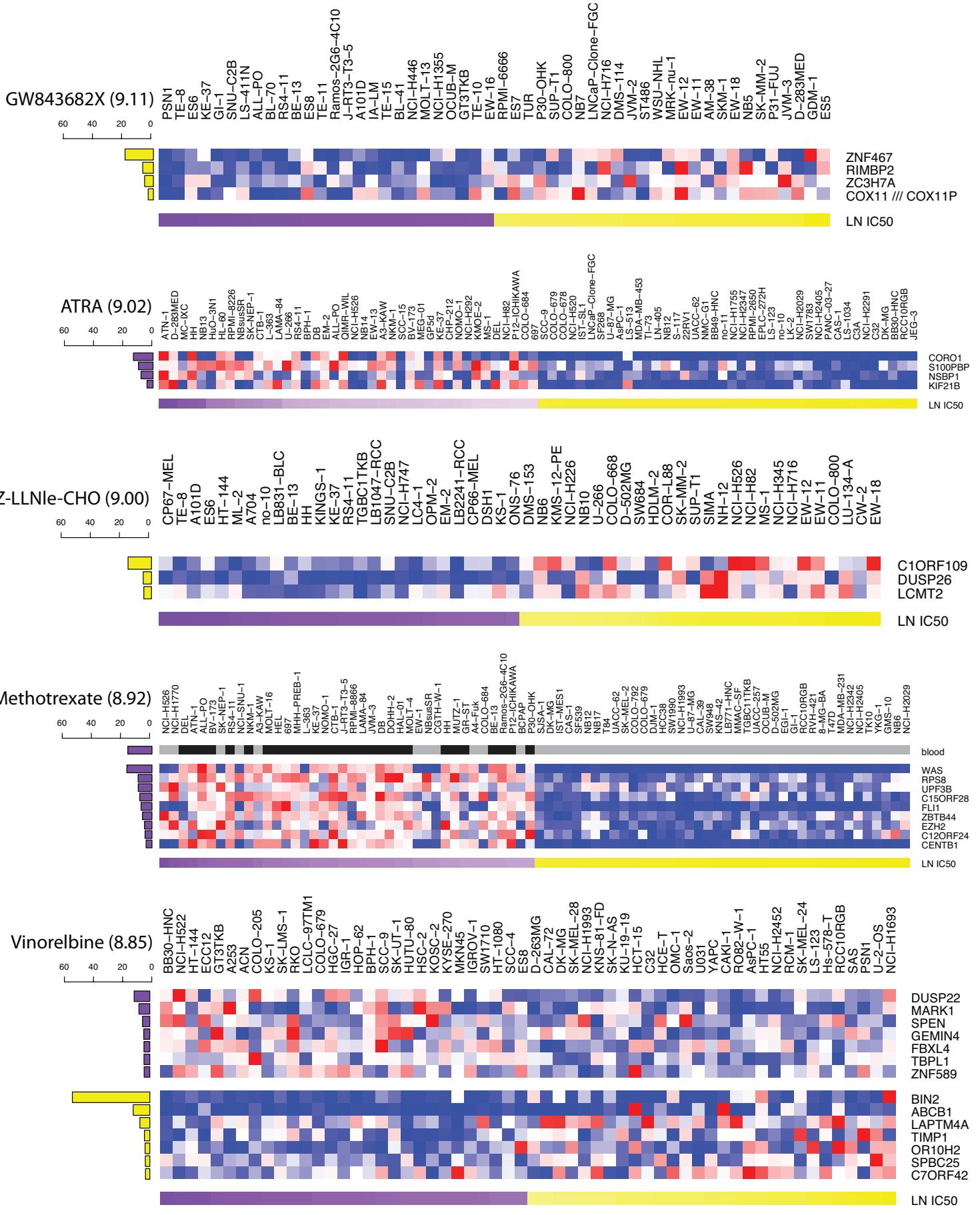
**Supplementary Figure 11: Decreased expression of apoptotic genes in *NOTCH1* mutant compared to wild-type hematopoietic cell.** Expression levels of the indicated genes were obtained from the U133A microarray dataset and statistical significance tested using student t-test. *NOTCH1* is frequently mutated in hematopoietic cell lines and so only cell lines of hematopoietic origin were considered to minimize tissue specific effects on expression (*NOTCH1* (MUT), n = 12; wild-type (WT), n = 80). Additional apoptotic regulators tested were not differentially expressed (*BAD*, *BBC3*, *BCL2L10*, *BID*, *BIK*, *BNIP1*, *BNIP2*, *BNIP3*, *MCL1*).

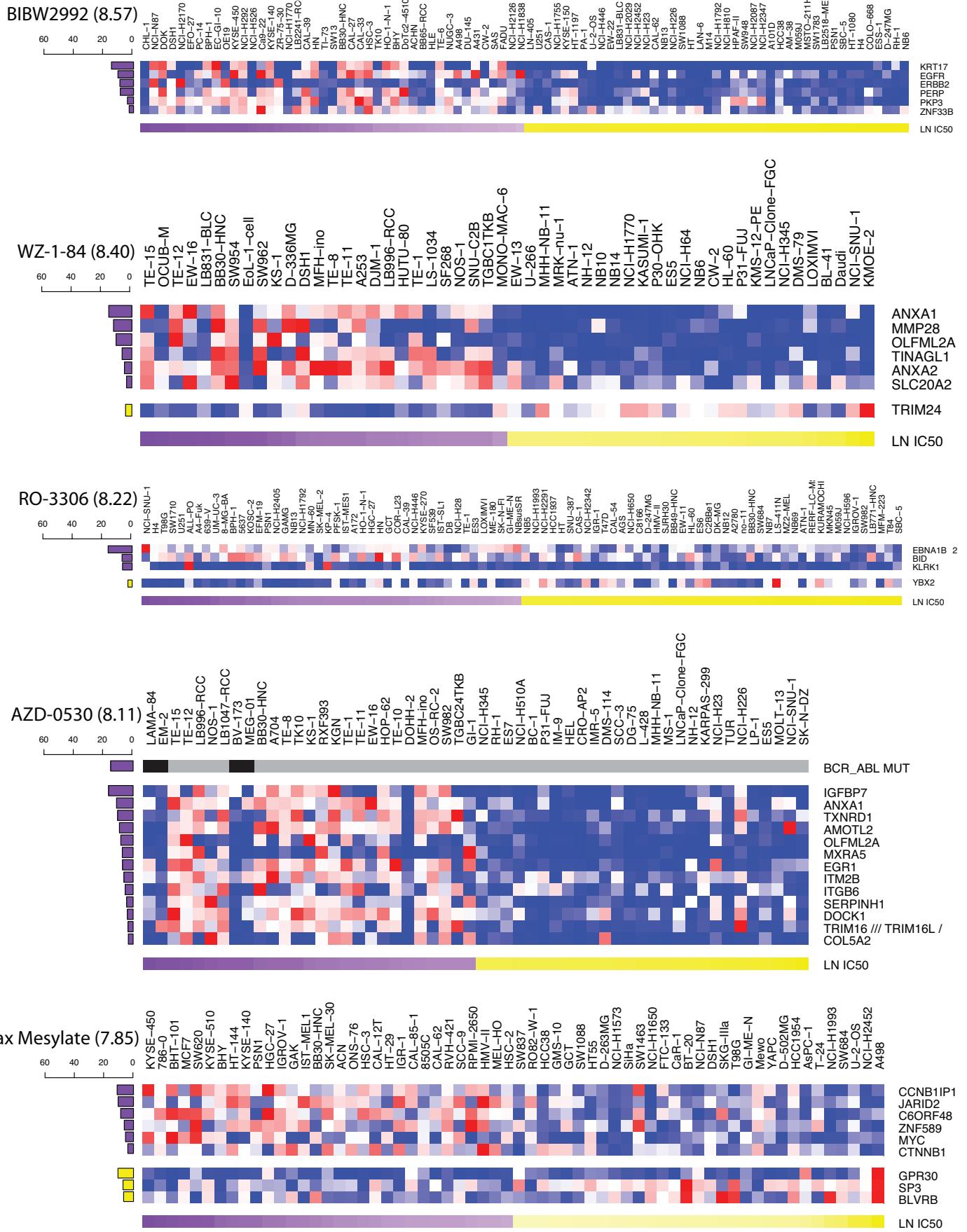


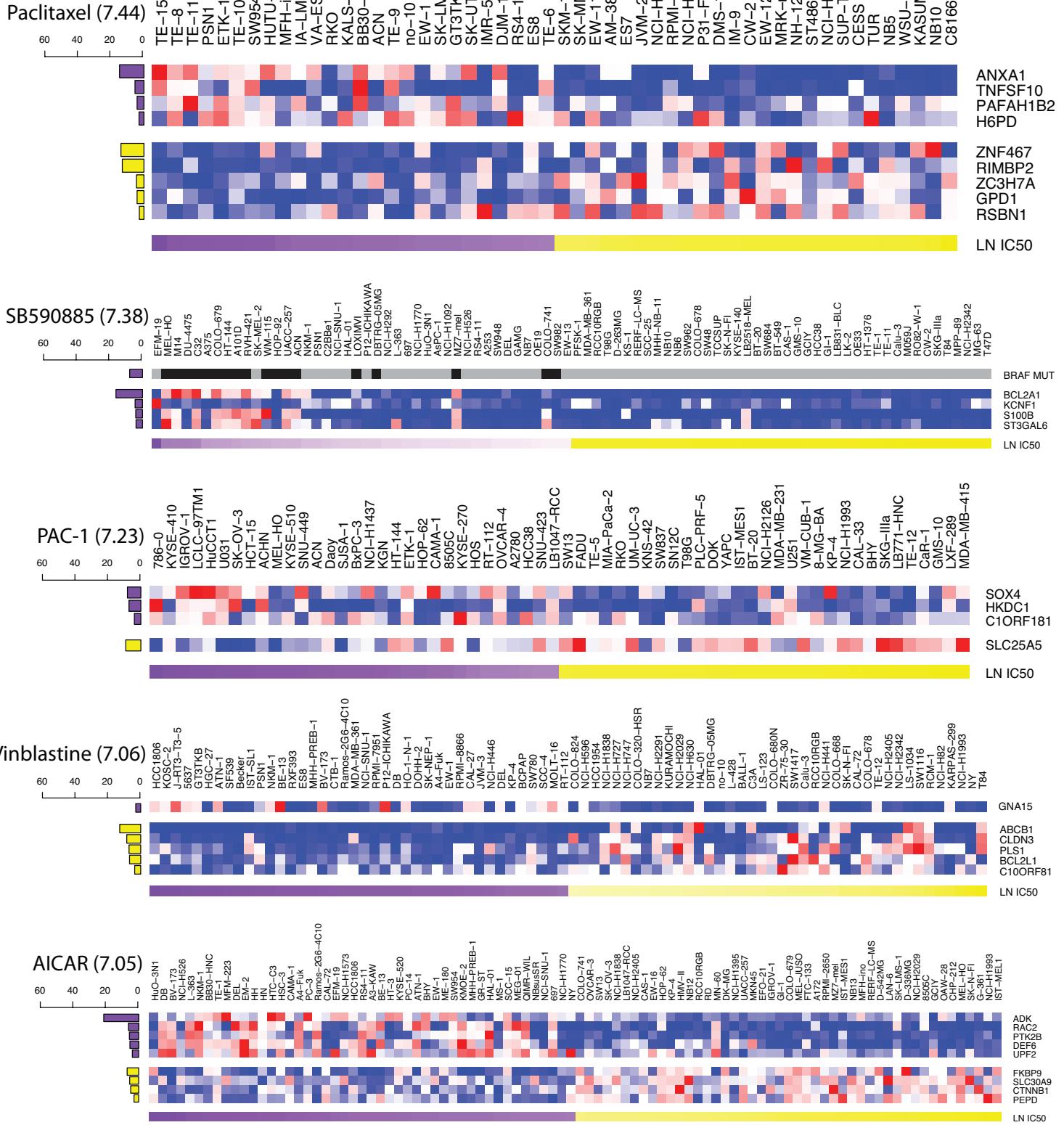
**Supplementary Figure 12: Sensitivity of SMAD4 mutated cell lines to EGFR inhibitors is associated with increased EGFR expression.** **a**, A scatter plot of *CCND1* mutated or wild-type (WT) cell line IC<sub>50</sub> values for BIBW2992 ( $P = 6.7 \times 10^{-4}$  from the MANOVA). Each circle represents the IC<sub>50</sub> of one cell line on a log scale and the red line is the geometric mean. **b**, *EGFR* gene expression is elevated in SMAD4 mutated cell lines ( $P = 0.0031$ , students t-test). A box and whisker plots of gene expression levels in wild-type (WT,  $n = 399$ ) cell lines or cell lines with a SMAD4 mutation ( $n = 24$ ). Whiskers indicate the 5th and 95th percentiles and outlier cell lines are indicated by black dots. Cell lines with *CCND1* mutation were also correlated with sensitivity to EGFR inhibitors from the MANOVA analysis but where not associated with altered *EGFR* gene expression. **c**, Cell line sensitivity to EGFR/ERBB2 inhibitor BIBW2992 is correlated with *EGFR* expression levels in WT (spearman correlation,  $r = -0.2051$ ,  $P < 0.0001$ ,  $n = 399$ ) and SMAD4 mutated ( $r = -0.5313$ ,  $P = 0.0075$ ,  $n = 24$ ) cell lines. Linear regressions for WT (black line) and SMAD4 mutated (red line) cell lines are shown. For the analysis in **b** and **c** all *EGFR* or *ERBB2* mutated cell lines were excluded.

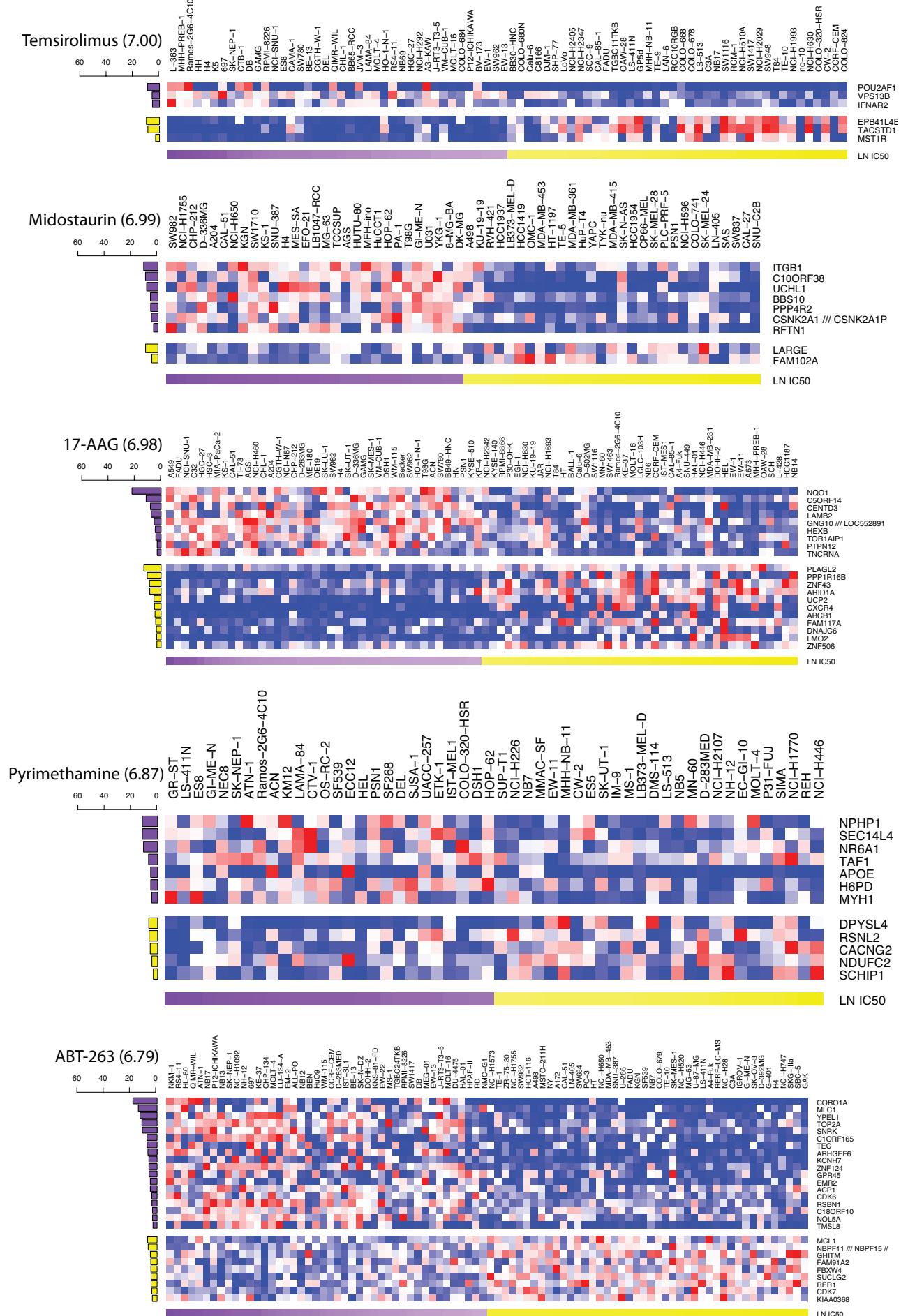


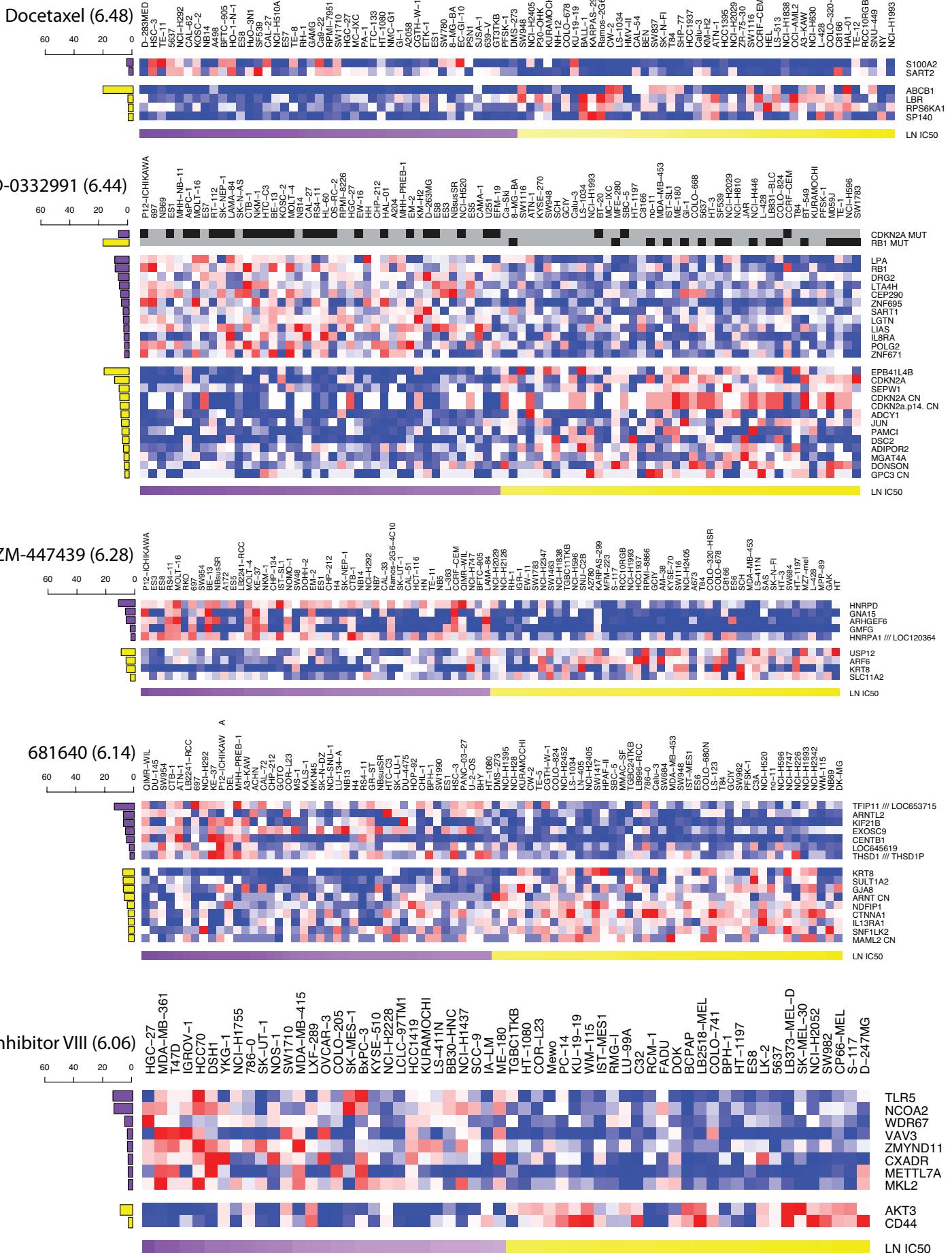


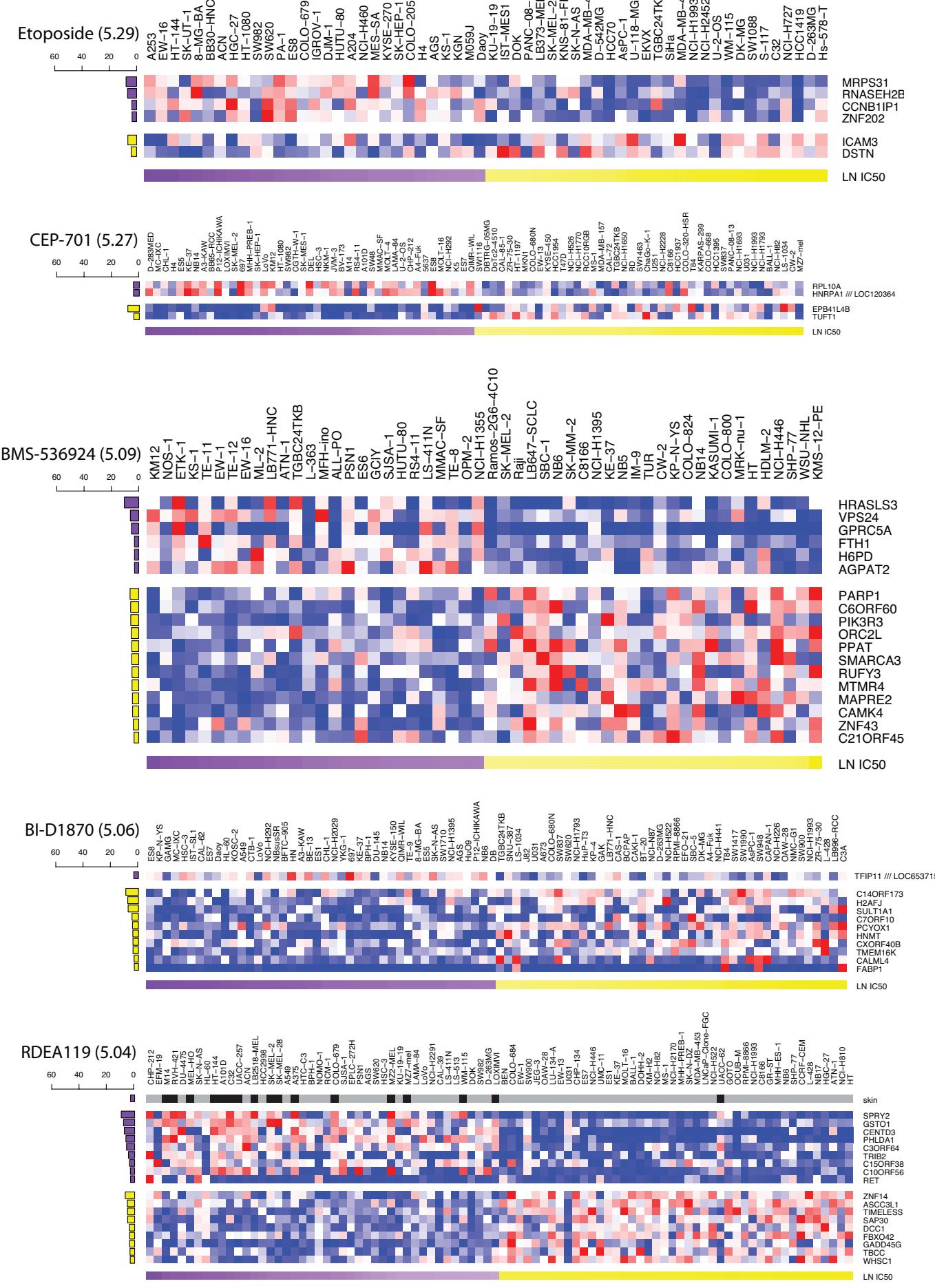




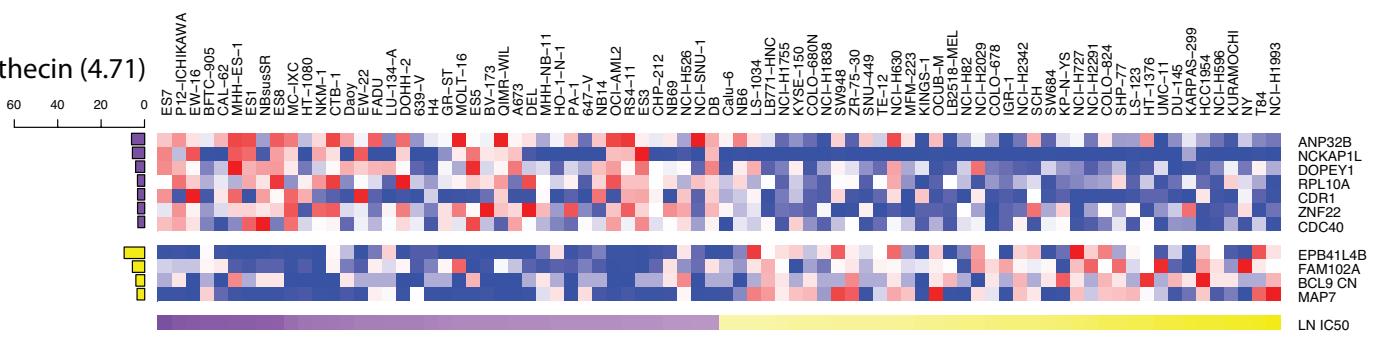




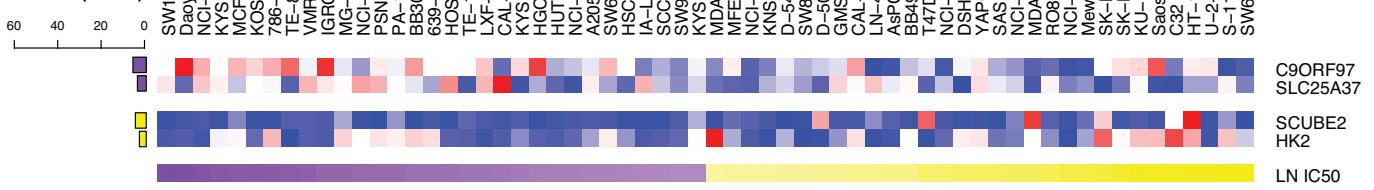




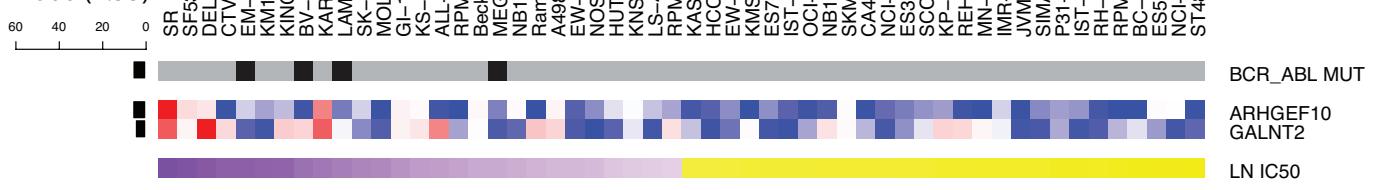
### Camptothecin (4.71)



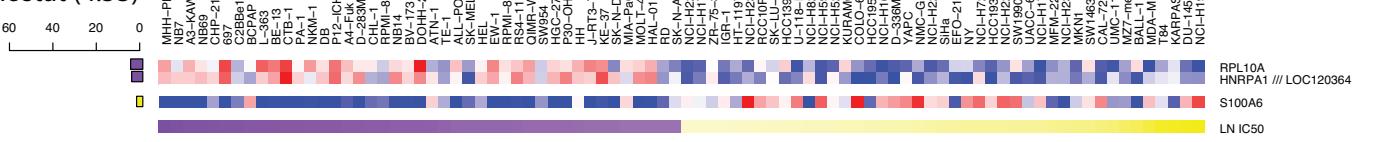
### Epothilone B (4.60)



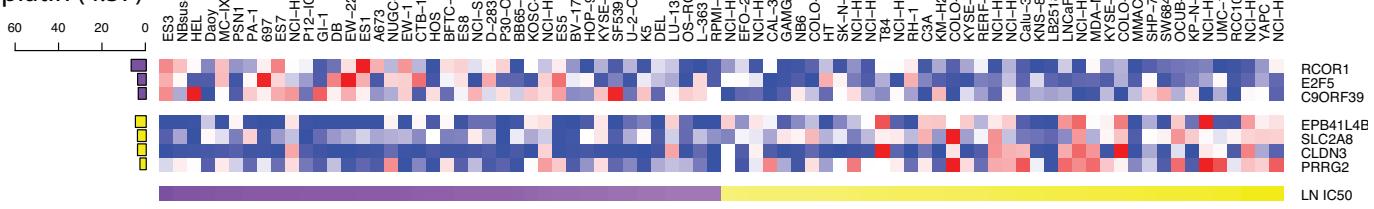
### PF-02341066 (4.55)

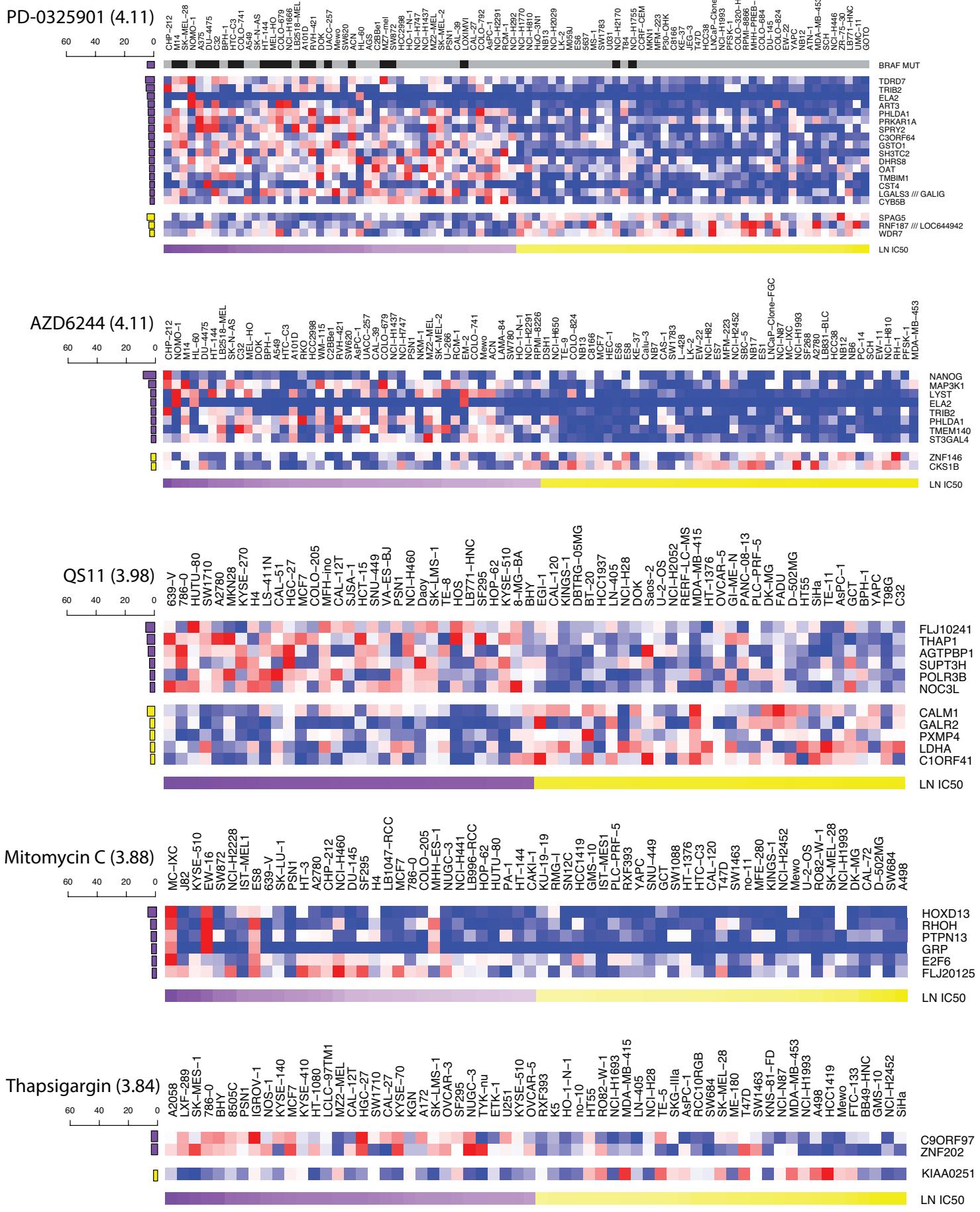


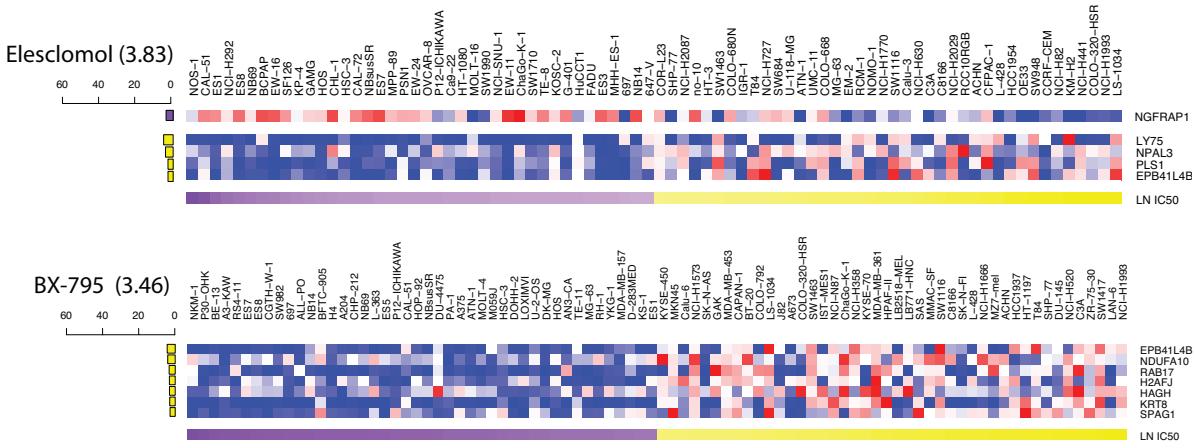
### Vorinostat (4.53)



### Cisplatin (4.37)



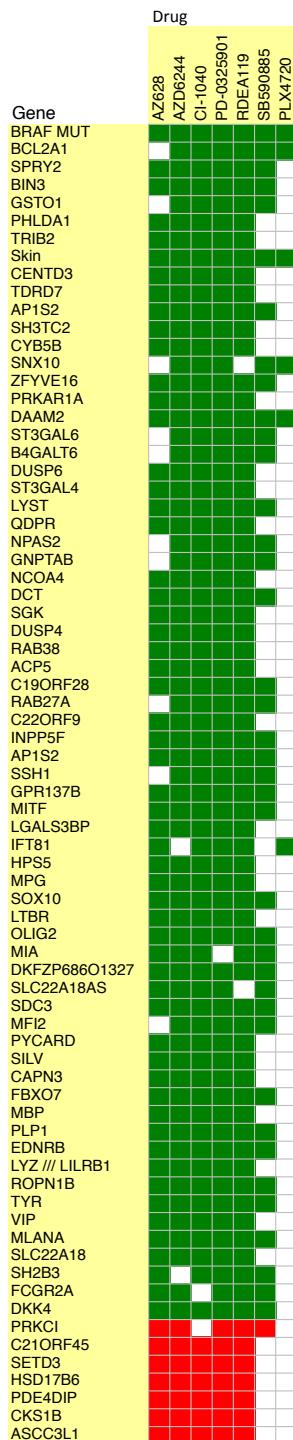




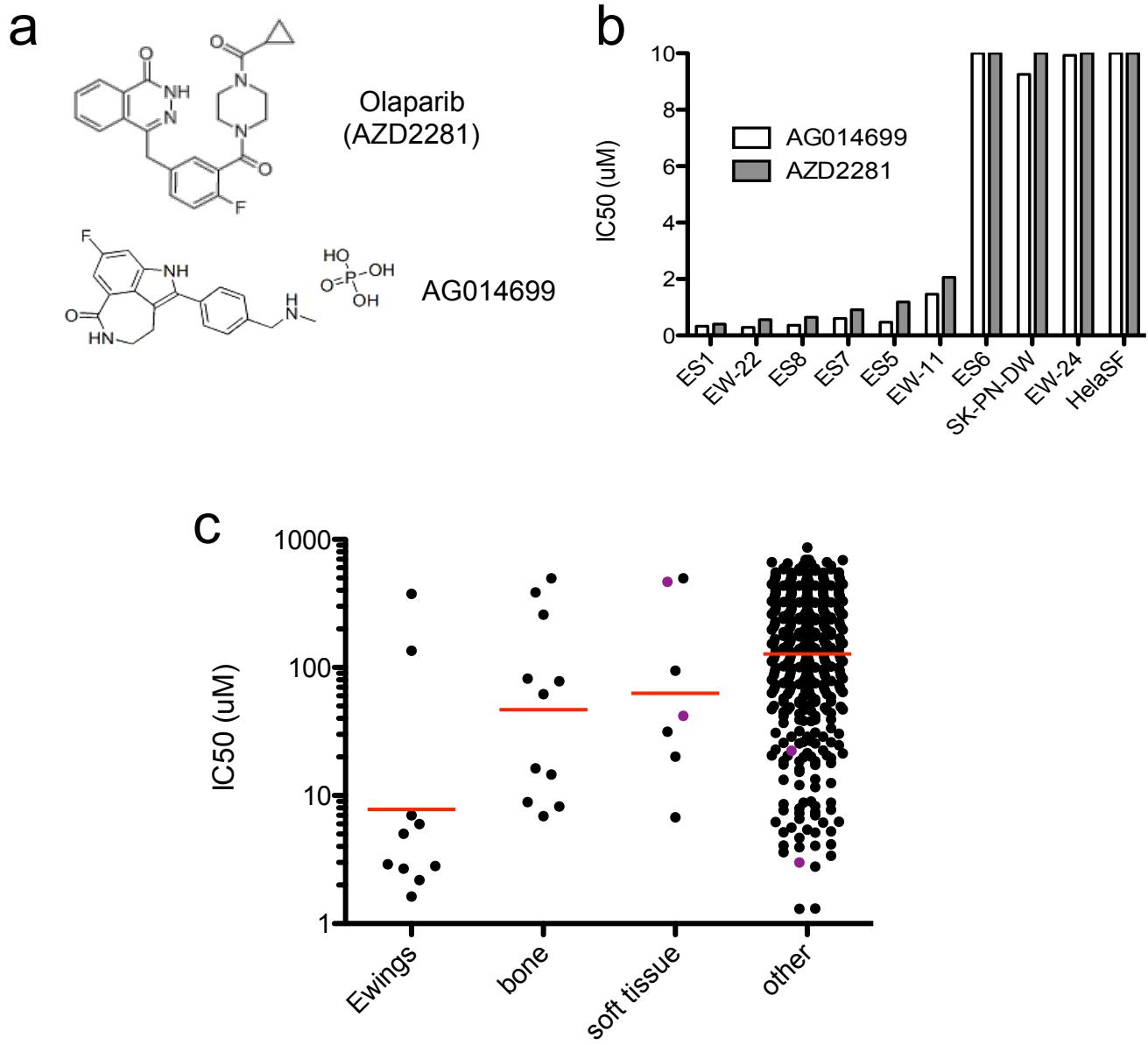
**Supplementary Figure 13:** Heatmaps for features in marker signatures of all drugs that have at least 2 features with significant effect sizes ( $-2.95 > e > 2.79$ ). Only features with significant effect sizes are shown. Mutation and tissue features are at the top of the heatmap shown in black (sample has feature) and gray (sample lacks feature) followed by sensitivity associated expression and copy number features and finally resistance associated expression and copy number features. To the left of each feature is a barplot indicating the absolute value of the effect size. Bars in purple are negative effects, indicating features associated with sensitivity and bars in yellow are positive effects, indicating features associated with resistance. The natural log IC50 for each cell line is represented at the bottom. Cell lines shown for each heatmap are those with lowest and highest 10% of IC50s for each drug.

Resistance					Sensitivity				
Genes	Drug	Target	Frequency	Effect	Gene	Drug	Target	Frequency	Effect
TP53 MUT	<b>Nutlin-3a</b>	MDM2	1	60.57	BCR_ABL MUT	<b>Dasatinib</b>	ABL, SRC, KIT, PDGFR	1	-61.29
BIN2	<b>Vinorelbine</b>	Microtubules	0.95	53.19		<b>Nilotinib</b>	ABL	1	-52.42
ZNF643	<b>MG-132</b>	Proteasome	1	21.95		<b>WH-4-023</b>	SRC, ABL	0.99	-43.69
RIMBP2	<b>JW-7-52-1</b>	MTOR	1	21.17		<b>Imatinib</b>	ABL, KIT, PDGFR	1	-28.72
	Paclitaxel	Microtubules	1	13.32		<b>GNF-2</b>	BCR-ABL	1	-22.63
	GW843682X	PLK1	0.99	7.34		<b>AZD-0530</b>	SRC, ABL	1	-15.34
ABCB1	<b>Docetaxel</b>	Microtubules	1	20.89		<b>PF-02341066</b>	MET, ALK	0.99	-4.88
	<b>Vinblastine</b>	Microtubules	1	12.91		<b>Axitinib</b>	PDGFR, KIT, VEGFR	1	-3.37
	Vinorelbine	Microtubules	1	11.40	LAG3	<b>GSK-650394</b>	SGK3	1	-29.90
	17-AAG	HSP90	1	4.62	MMP28	<b>Lapatinib</b>	EGFR, ERBB2	1	-27.54
ZNF467	<b>GW843682X</b>	PLK1	0.99	19.48		<b>WZ-1-84</b>	BMX	1	-12.54
	<b>Paclitaxel</b>	Microtubules	1	14.17	ERBB2	<b>Lapatinib</b>	EGFR, ERBB2	1	-26.41
	BI-2536	PLK1/2/3	0.85	8.23		<b>BIBW2992</b>	EGFR, ERBB2	1	-9.34
RB1 MUT	<b>PD-0332991</b>	CDK4/6	1	18.10	PERLD1	<b>Lapatinib</b>	EGFR, ERBB2	1	-23.70
EPB41L4B	<b>PD-0332991</b>	CDK4/6	1	17.34	BRAF MUT	<b>PLX4720</b>	BRAF	1	-23.25
	Temsirolimus	MTOR	1	10.00		<b>SB590885</b>	BRAF	1	-7.89
	Camptothecin	TOP1	1	9.48		<b>PD-0325901</b>	MEK1/2	1	-4.99
	CEP-701	FLT3, JAK2, NTRK1, RET	1	8.43	NQO1	<b>17-AAG</b>	HSP90	1	-22.21
	NVP-BEZ235	PI3K /mTor	0.97	8.35	ADK	<b>AICAR</b>	AMPK agonist	1	-21.52
	Cisplatin	DNA crosslinker	1	5.00	CDKN2a(p14) MUT	<b>Dasatinib</b>	ABL, SRC, KIT, PDGFR	1	-20.28
	BX-795	TBK1, PDK1, IKK, AURKB/C	1	4.44		<b>WH-4-023</b>	SRC, ABL	0.99	-11.93
	Elesclomol	HSP70	1	2.85	PCSK5	<b>Erlotinib</b>	EGFR	1	-19.60
C1ORF109	<b>Z-LNN1e-CHO</b>	g-secretase	1	16.09	TRIM16	Dasatinib	ABL, SRC, KIT, PDGFR	1	-19.27
CCNT2	<b>Dasatinib</b>	ABL, SRC, KIT, PDGFR	1	15.96		<b>AZD-0530</b>	SRC, ABL	1	-3.52
GARNL1	<b>MG-132</b>	Proteasome	1	14.91					
PLAGL2	<b>17-AAG</b>	HSP90	1	13.14					

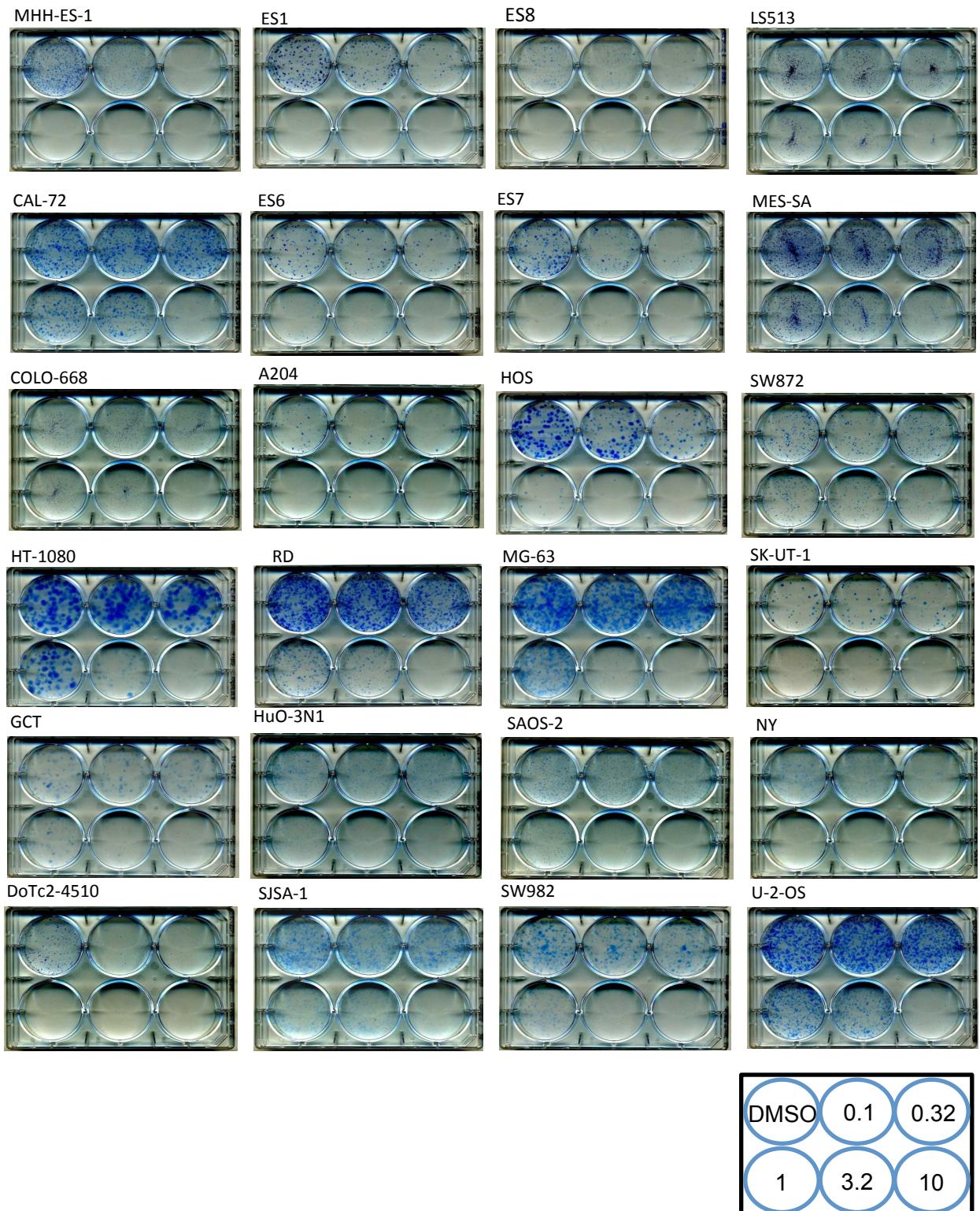
**Supplementary Table 3: Highly significant genomic biomarkers of drug response from EN analysis.** High frequency features ( $f > 0.76$ ) associated with the largest effect sizes are displayed together with the relevant drug and grouped into positive effect sizes associated with resistance (left) and negative effect sizes associated with sensitivity (right). The top 15 resistance and sensitivity associations are in bold and additional drugs that are associated with each gene at the significance criteria are included in the table.



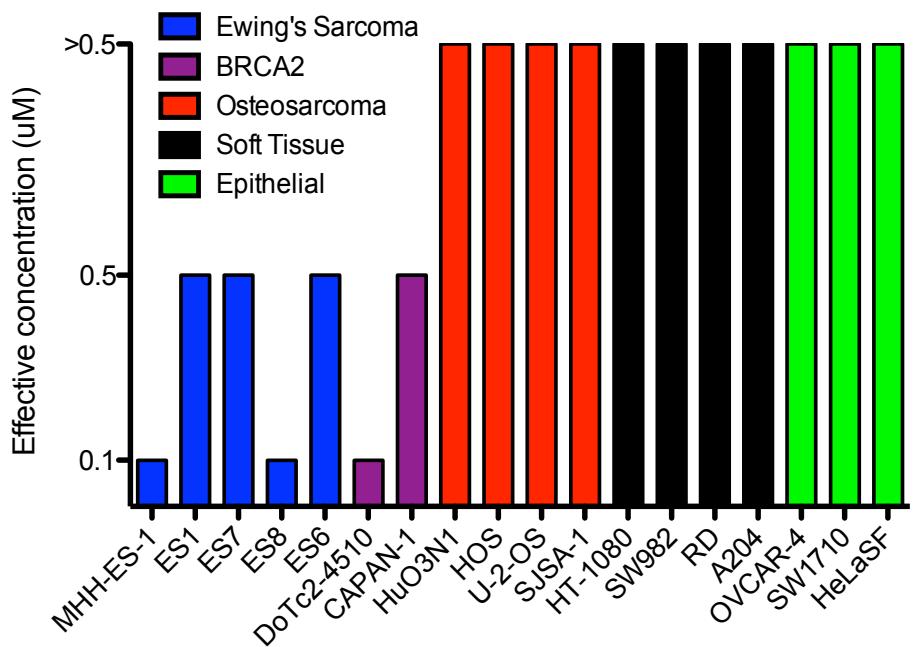
**Supplementary Figure 14: Heatmap of recurrent features in RAF and MEK1/2 inhibitor signatures from EN analysis.** Green indicates that the feature is associated with drug sensitivity and red indicates association with resistance. Features displayed were present in 5 or more of the 7 RAF and MEK1/2 inhibitors screened.



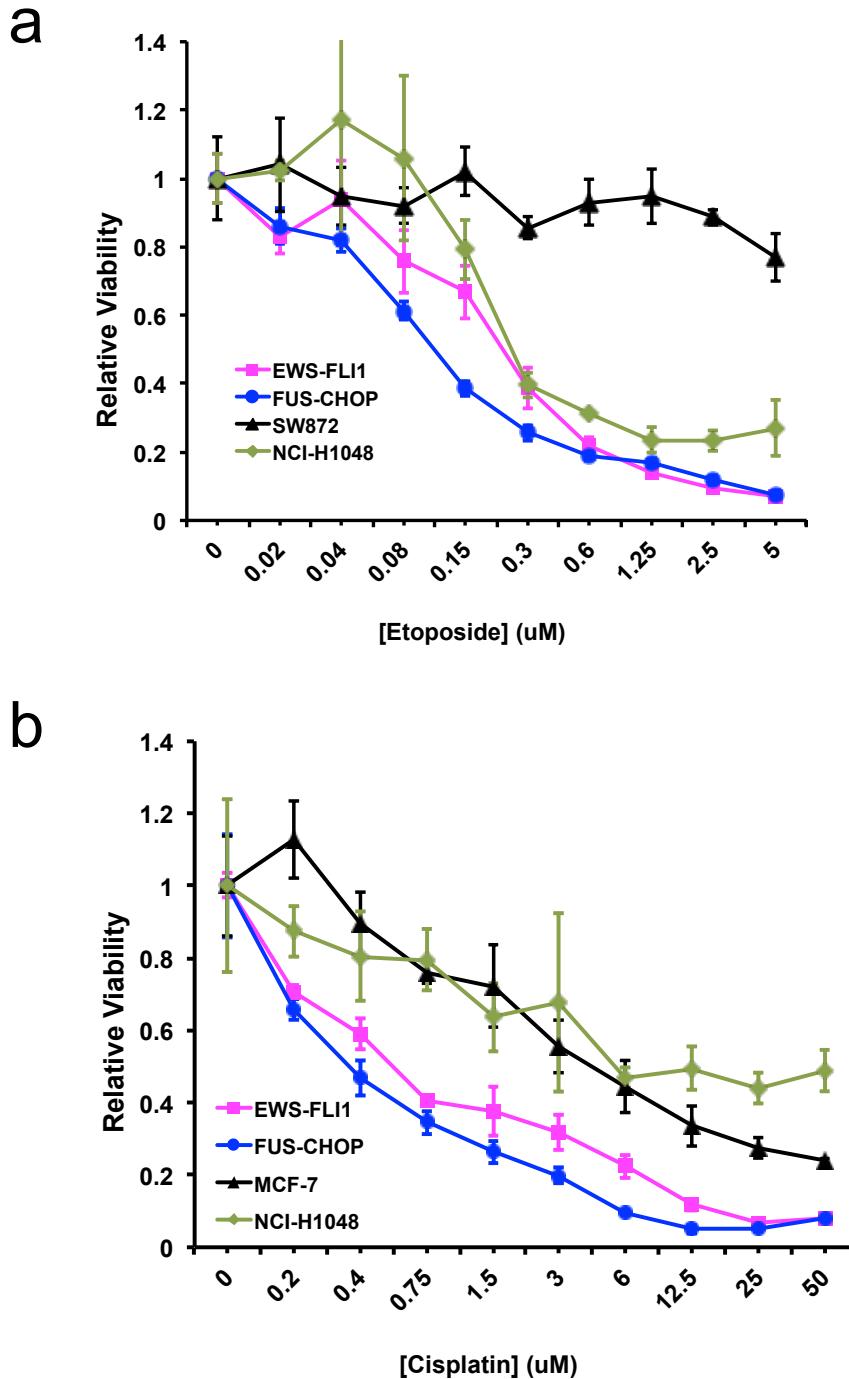
**Supplementary Figure 15: Ewing's sarcoma cells are sensitive to multiple PARP inhibitors.** **a**, Chemical structures of PARP inhibitors olaparib and AG014699 used in this study. **b**, Comparison of IC<sub>50</sub> values of Ewing's cells to olaparib and AG014699 in a 6-day viability assay. IC<sub>50</sub> values are capped at 10 μM and HeLaSF cells are included as a negative control. The majority of Ewing's sarcoma cells are acutely sensitive to PARP inhibitors but some cells do not respond in this assay. **c**, Ewing's sarcoma cells show marked sensitivity to olaparib compared to other bone and soft tissue cancers. A scatter plot of cell line IC<sub>50</sub> values ( $n = 459$ ) to olaparib on a log scale is shown and the red line indicates the geometric mean. Purple circles are cell lines which have the *EWS-FLI1* rearrangement but historically have not been classified histologically as Ewing's.



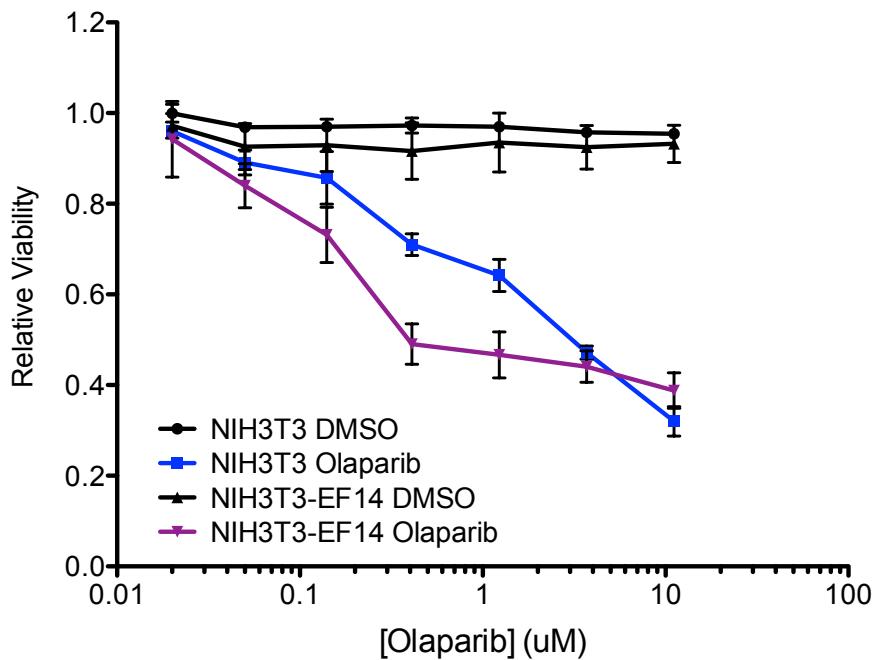
**Supplementary Figure 16: Images of olaparib clonogenic assays for Ewing's sarcoma and control cell lines.** Clonogenic assays were performed in the presence of increasing concentrations of olaparib (0.1, 0.32, 1, 3.2 or 10 uM final concentration). Plates were re-drugged every 4 days and fixed and stained 7-21 days following plating. The name of each cell line is given and a schematic (lower right) shows the concentration used for each well.



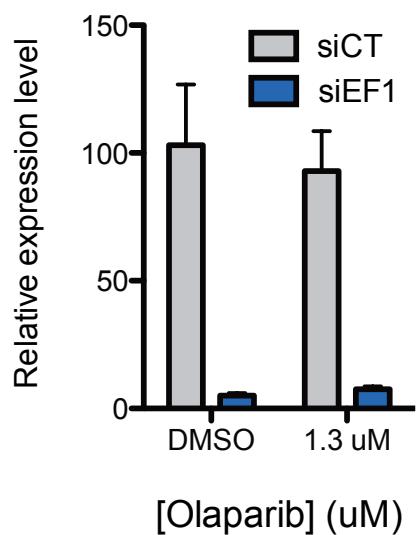
**Supplementary Figure 17: Ewing's sarcoma cells are sensitive to PARP inhibitor AG014699 in colony formation assays.** Cell lines were treated with 0.1  $\mu\text{M}$  or 0.5  $\mu\text{M}$  AG014699 for 7-21 days with re-druging every 3-4 days. For each cell line the concentration necessary to reduce colonies >90% relative to controls is plotted.



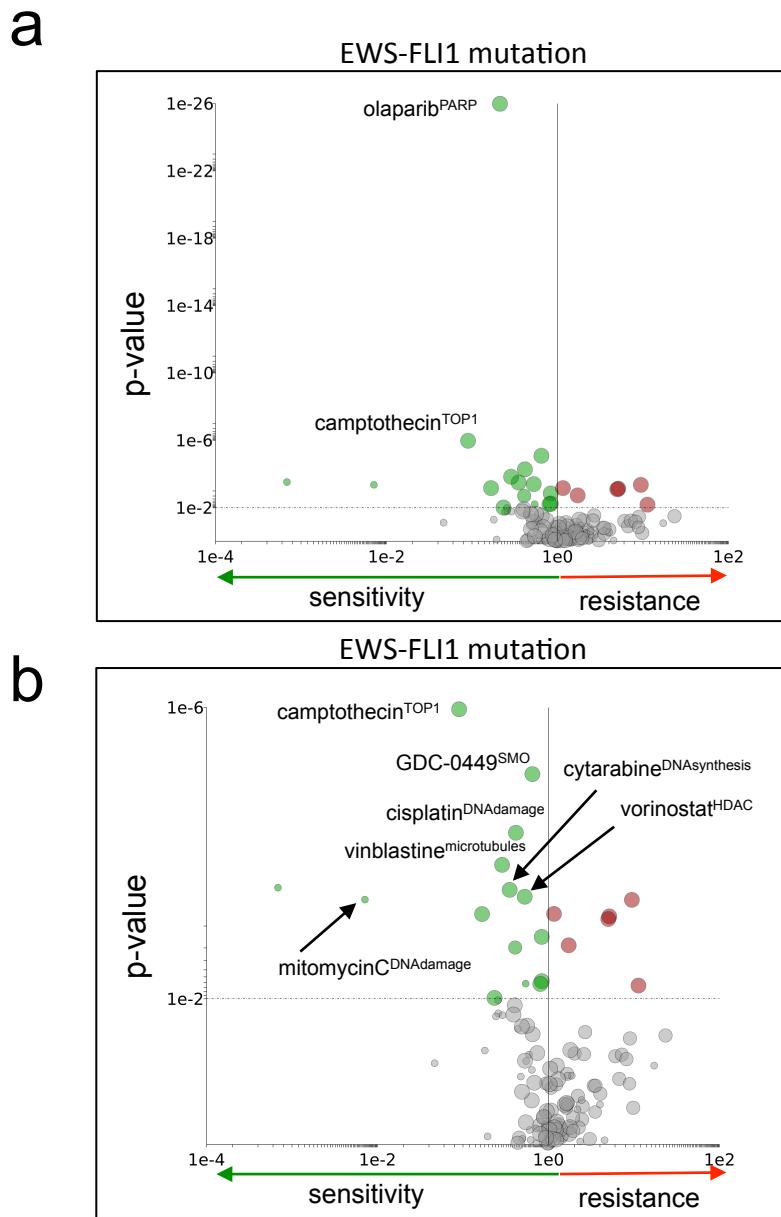
**Supplementary Figure 18: *EWS-FLI1* transformed mouse mesenchymal cells are not sensitised to etoposide or cisplatin.** As a control we show dose response curves to **a**, etoposide or **b**, cisplatin comparing the sensitivity of *EWS-FLI1* and *FUS-CHOP* transformed mouse mesenchymal cell lines. Human non-mesenchymal cell lines were included as an additional control. Each drug concentration was assayed in triplicate and error bars represent s.d.



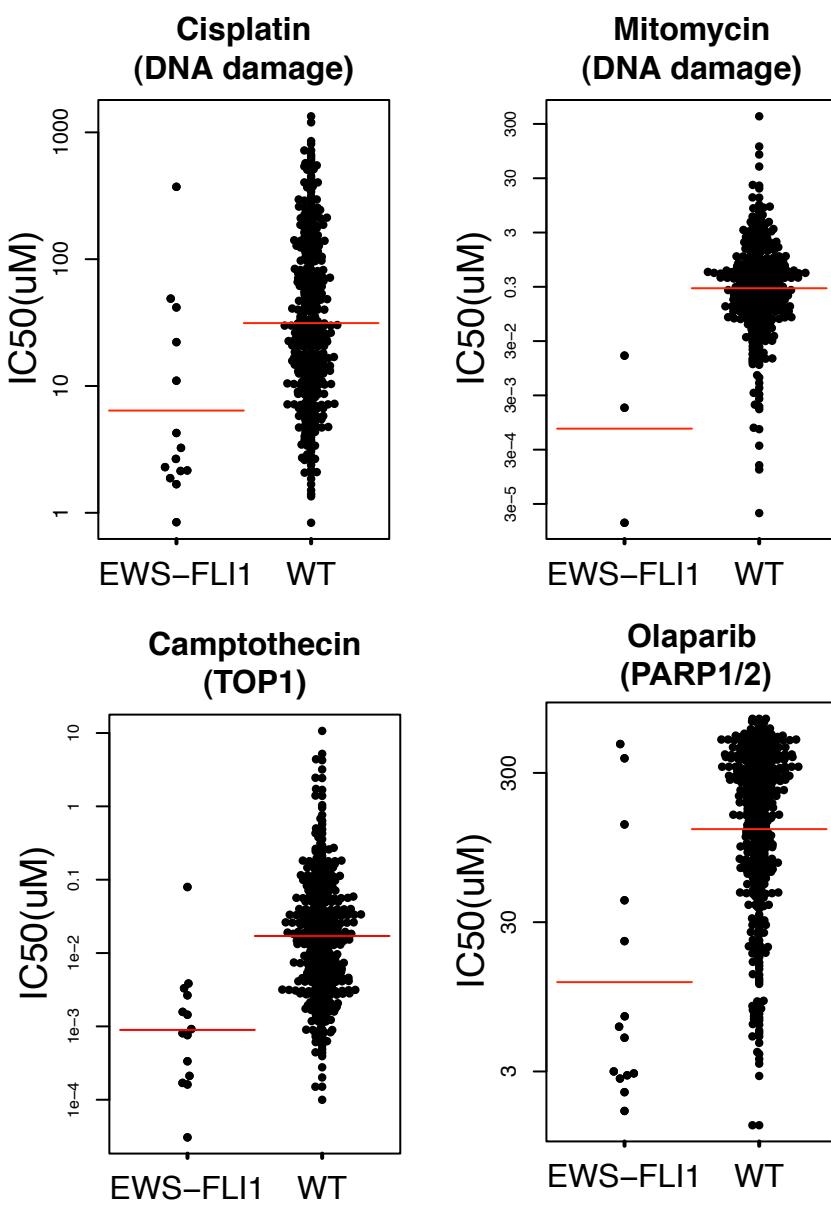
**Supplementary Figure 19: EWS-FLI1 expression is specifically associated with PARP inhibitor sensitivity.** Olaparib dose response curves of NIH3T3 cells stably expressing EWS-FLI1 (NIH3T3-EF14) or the parental control line. Expression of EWS-FLI1 increased sensitivity to olaparib. The effect was greatest at low doses of olaparib whereas at higher doses both cell lines were sensitive presumably due to general cellular toxicity. Viability was normalised to untreated cells. Each drug concentration was assayed in triplicate and error bars represent the s.d.



**Supplementary Figure 20: Confirmation of siRNA-mediated depletion of EWS-FLI1 in A673 cells.** A673 were transfected with either control (siCT) or EWS-FLI1 (siEF1) siRNA for 72 hours and cells were concomitantly treated with either olaparib or DMSO. Relative expression levels of EWS-FLI1 (normalized to ribosomal protein RPLP0) were assessed by RT-QPCR. Expression was assayed in triplicate and errors bars are s.d.



**Supplementary Figure 21: The *EWS-FLI1* rearrangement is associated with sensitivity to cytotoxic drugs.** **a** and **b**, *EWS-FLI1* mutation-specific volcano plots of drug sensitivity from MANOVA. The drug name is indicated and therapeutic drug target(s) (in superscript) are indicated for selected data. Circle size is proportional to the number of mutant cell lines screened (max = 14 for **a** and **b**). For **b** the data for olaparib has been removed to make less significant associations clear (note the change to scaling on y-axis).



**Supplementary Figure 22: Association of the *EWS-FLI1* translocation with sensitivity to DNA damaging agents.** Scatter plots of  $IC_{50}$  values from selected associations from the MANOVA of *EWS-FLI1* with cytotoxic drugs. The data for olaparib (AZD-2281) is also included for comparison. The cell line  $IC_{50}$  values ( $\mu M$ ) for each drug are given comparing mutated (MUT) or non-mutated (WT) cell lines. Each circle represents the  $IC_{50}$  of one cell line plotted on a log scale and the red bar is the geometric mean. The drug name is indicated above each plot and target(s) are given in brackets.